

SEQUENCE LISTING

<110> Paszty, Christopher J.
Gong, Jianhua
Daugherty, Betsy
Rogers, Norma

<120> Leucine-Rich G Protein Coupled Receptor-8 Molecules and
Uses Thereof

<130> 00-1229

<140>

<141>

<150> 60/224,455

<151> 2000-08-10

<160> 42

<170> PatentIn Ver. 2.0

<210> 1

<211> 2265

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2262)

<220>

<221> sig_peptide

<222> (1)..(108)

<400> 1

atg att gtt ttt ctg gtt ttt aaa cat ctc ttc agc ctc aga ttg att	48
Met Ile Val Phe Leu Val Phe Lys His Leu Phe Ser Leu Arg Leu Ile	
1 5 10 15	

aca atg ttc ttt cta ctt cat ttc atc gtt ctg atc aat gtc aaa gat	96
Thr Met Phe Phe Leu Leu His Phe Ile Val Leu Ile Asn Val Lys Asp	
20 25 30	

ttt gca ctg act caa ggt agc atg atc act cct tca tgc caa aaa gga	144
Phe Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly	
35 40 45	

tat ttt ccc tgt ggg aat ctt acc aag tgc tta ccc cga gct ttt cac	192
Tyr Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His	
50 55 60	

tgt gat ggc aag gat gac tgt ggg aac ggg gcg gac gaa gag aac tgt	240
Cys Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys	
65 70 75 80	

ggg gac act agt gga tgg gcg acc ata ttt ggc aca gtg cat gga aat	288
---	-----

Gly	Asp	Thr	Ser	Gly	Trp	Ala	Thr	Ile	Phe	Gly	Thr	Val	His	Gly	Asn	
				85					90					95		
gct	aac	agc	gtg	gcc	tta	aca	cag	gag	tgc	ttt	cta	aaa	cag	tat	cca	336
Ala	Asn	Ser	Val	Ala	Leu	Thr	Gln	Glu	Cys	Phe	Leu	Lys	Gln	Tyr	Pro	
			100					105					110			
caa	tgc	tgt	gac	tgc	aaa	gaa	act	gaa	ttg	gaa	tgt	gta	aat	ggg	gac	384
Gln	Cys	Cys	Asp	Cys	Lys	Glu	Thr	Glu	Leu	Glu	Cys	Val	Asn	Gly	Asp	
		115					120					125				
tta	aag	tct	gtg	ccg	atg	att	tct	aac	aat	gtg	aca	tta	ctg	tct	ctt	432
Leu	Lys	Ser	Val	Pro	Met	Ile	Ser	Asn	Asn	Val	Thr	Leu	Leu	Ser	Leu	
	130					135					140					
aag	aaa	aac	aaa	atc	cac	agt	ctt	cca	gat	aaa	ggt	ttc	atc	aaa	tac	480
Lys	Lys	Asn	Lys	Ile	His	Ser	Leu	Pro	Asp	Lys	Val	Phe	Ile	Lys	Tyr	
145				150						155					160	
aca	aaa	ctt	aaa	aag	ata	ttt	ctt	cag	cat	aat	tgc	att	aga	cac	ata	528
Thr	Lys	Leu	Lys	Lys	Ile	Phe	Leu	Gln	His	Asn	Cys	Ile	Arg	His	Ile	
			165					170					175			
tcc	agg	aaa	gca	ttt	ttt	gga	tta	tgt	aat	ctg	caa	ata	tta	tat	ctc	576
Ser	Arg	Lys	Ala	Phe	Phe	Gly	Leu	Cys	Asn	Leu	Gln	Ile	Leu	Tyr	Leu	
			180					185					190			
aac	cac	aac	tgc	atc	aca	acc	ctc	aga	cct	gga	ata	ttc	aaa	gac	tta	624
Asn	His	Asn	Cys	Ile	Thr	Thr	Leu	Arg	Pro	Gly	Ile	Phe	Lys	Asp	Leu	
		195					200					205				
cat	cag	cta	act	tgg	cta	att	cta	gat	gac	aat	cca	ata	acc	aga	att	672
His	Gln	Leu	Thr	Trp	Leu	Ile	Leu	Asp	Asp	Asn	Pro	Ile	Thr	Arg	Ile	
	210					215					220					
tca	cag	cgc	ttg	ttt	acg	gga	tta	aat	tcc	ttg	ttt	ttc	ctg	tct	atg	720
Ser	Gln	Arg	Leu	Phe	Thr	Gly	Leu	Asn	Ser	Leu	Phe	Phe	Leu	Ser	Met	
225				230					235						240	
gtt	aat	aac	tac	tta	gaa	gct	ctt	ccc	aag	cag	atg	tgt	gcc	caa	atg	768
Val	Asn	Asn	Tyr	Leu	Glu	Ala	Leu	Pro	Lys	Gln	Met	Cys	Ala	Gln	Met	
			245					250					255			
cct	caa	ctc	aac	tgg	gtg	gat	ttg	gaa	ggc	aat	aga	ata	aag	tat	ctc	816
Pro	Gln	Leu	Asn	Trp	Val	Asp	Leu	Glu	Gly	Asn	Arg	Ile	Lys	Tyr	Leu	
			260				265						270			
aca	aat	tct	acg	ttt	ctg	tcg	tgc	gat	tcg	ctc	aca	gtg	ctg	ttt	ctg	864
Thr	Asn	Ser	Thr	Phe	Leu	Ser	Cys	Asp	Ser	Leu	Thr	Val	Leu	Phe	Leu	
		275					280					285				
cct	aga	aat	caa	att	ggg	ttt	gtt	cca	gag	aag	aca	ttt	tct	tca	tta	912
Pro	Arg	Asn	Gln	Ile	Gly	Phe	Val	Pro	Glu	Lys	Thr	Phe	Ser	Ser	Leu	
	290					295					300					
aaa	aat	tta	gga	gaa	ctg	gat	ctg	tct	agc	aat	acg	ata	acg	gag	cta	960
Lys	Asn	Leu	Gly	Glu	Leu	Asp	Leu	Ser	Ser	Asn	Thr	Ile	Thr	Glu	Leu	

305	310	315	320	
tca cct cac ctt ttt aaa gac ttg aag ctt cta caa aag ctg aac ctg				1008
Ser Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asn Leu	325	330	335	
tca tcc aat cct ctt atg tat ctt cac aag aac cag ttt gaa agt ctt				1056
Ser Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln Phe Glu Ser Leu	340	345	350	
aaa caa ctt cag tct cta gac ctg gaa agg ata gag att cca aat ata				1104
Lys Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile	355	360	365	
aac aca cga atg ttt caa ccc atg aag aat ctt tct cac att tat ttc				1152
Asn Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe	370	375	380	
aaa aac ttt cga tac tgc tcc tat gct ccc cat gtc cga ata tgt atg				1200
Lys Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val Arg Ile Cys Met	385	390	400	
ccc ttg acg gac ggc att tct tca ttt gag gac ctc ttg gct aac aat				1248
Pro Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn	405	410	415	
atc ctc aga ata ttt gtc tgg gtt ata gct ttc att acc tgc ttt gga				1296
Ile Leu Arg Ile Phe Val Trp Val Ile Ala Phe Ile Thr Cys Phe Gly	420	425	430	
aat ctt ttt gtc att ggc atg aga tct ttc att aaa gct gaa aat aca				1344
Asn Leu Phe Val Ile Gly Met Arg Ser Phe Ile Lys Ala Glu Asn Thr	435	440	445	
act cac gct atg tcc atc aaa atc ctt tgt tgt gct gat tgc ctg atg				1392
Thr His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala Asp Cys Leu Met	450	455	460	
ggt gtt tac ttg ttc ttt gtt ggc att ttc gat ata aaa tac cga ggg				1440
Gly Val Tyr Leu Phe Phe Val Gly Ile Phe Asp Ile Lys Tyr Arg Gly	465	470	480	
cag tat cag aag tat gcc ttg ctg tgg atg gag agc gtg cag tgc cgc				1488
Gln Tyr Gln Lys Tyr Ala Leu Leu Trp Met Glu Ser Val Gln Cys Arg	485	490	495	
ctc atg ggg ttc ctg gcc atg ctg tcc acc gaa gtc tct gtt ctg cta				1536
Leu Met Gly Phe Leu Ala Met Leu Ser Thr Glu Val Ser Val Leu Leu	500	505	510	
ctg acc tac ttg act ttg gag aag ttc ctg gtc att gtc ttc ccc ttc				1584
Leu Thr Tyr Leu Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe	515	520	525	
agt aac att cga cct gga aaa cgg cag acc tca gtc atc ctc att tgc				1632
Ser Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile Cys	530	535	540	

atc tgg atg gcg gga ttt tta ata gct gta att cca ttt tgg aat aag	1680
Ile Trp Met Ala Gly Phe Leu Ile Ala Val Ile Pro Phe Trp Asn Lys	
545 550 555 560	
gat tat ttt gga aac ttt tat ggg aaa aat gga gta tgt ttc cca ctt	1728
Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu	
565 570 575	
tat tat gac caa aca gaa gat att gga agc aaa ggg tat tct ctt gga	1776
Tyr Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser Leu Gly	
580 585 590	
att ttc cta ggt gtg aac ttg ctg gct ttt ctc atc att gtg ttt tcc	1824
Ile Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Ile Ile Val Phe Ser	
595 600 605	
tat att act atg ttc tgt tcc att caa aaa acc gcc ttg cag acc aca	1872
Tyr Ile Thr Met Phe Cys Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr	
610 615 620	
gaa gta agg aat tgt ttt gga aga gag gtg gct gtt gca aat cgt ttc	1920
Glu Val Arg Asn Cys Phe Gly Arg Glu Val Ala Val Ala Asn Arg Phe	
625 630 635 640	
ttt ttt ata gtg ttc tct gat gcc atc tgc tgg att cct gta ttt gta	1968
Phe Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val	
645 650 655	
gtt aaa atc ctt tcc ctc ttc cgg gtg gaa ata cca gac aca atg act	2016
Val Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro Asp Thr Met Thr	
660 665 670	
tcc tgg ata gtg att ttt ttc ctt cca gtt aac agt gct ttg aat cca	2064
Ser Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro	
675 680 685	
atc ctc tat act ctc aca acc aac ttt ttt aag gac aag ttg aaa cag	2112
Ile Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln	
690 695 700	
ctg ctg cac aaa cat cag agg aaa tca att ttc aaa att aaa aaa	2160
Leu Leu His Lys His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys	
705 710 715 720	
agt tta tct aca tcc att gtg tgg ata gag gac tcc tct tcc ctg aaa	2208
Ser Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu Lys	
725 730 735	
ctt ggg gtt ttg aac aaa ata aca ctt gga gac agt ata atg aaa cca	2256
Leu Gly Val Leu Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro	
740 745 750	
gtt tcc tag	2265
Val Ser	

<210> 2
 <211> 754
 <212> PRT
 <213> Homo sapiens

<400> 2

Met	Ile	Val	Phe	Leu	Val	Phe	Lys	His	Leu	Phe	Ser	Leu	Arg	Leu	Ile	1	5	10	15
Thr	Met	Phe	Phe	Leu	Leu	His	Phe	Ile	Val	Leu	Ile	Asn	Val	Lys	Asp	20	25	30	
Phe	Ala	Leu	Thr	Gln	Gly	Ser	Met	Ile	Thr	Pro	Ser	Cys	Gln	Lys	Gly	35	40	45	
Tyr	Phe	Pro	Cys	Gly	Asn	Leu	Thr	Lys	Cys	Leu	Pro	Arg	Ala	Phe	His	50	55	60	
Cys	Asp	Gly	Lys	Asp	Asp	Cys	Gly	Asn	Gly	Ala	Asp	Glu	Glu	Asn	Cys	65	70	75	80
Gly	Asp	Thr	Ser	Gly	Trp	Ala	Thr	Ile	Phe	Gly	Thr	Val	His	Gly	Asn	85	90	95	
Ala	Asn	Ser	Val	Ala	Leu	Thr	Gln	Glu	Cys	Phe	Leu	Lys	Gln	Tyr	Pro	100	105	110	
Gln	Cys	Cys	Asp	Cys	Lys	Glu	Thr	Glu	Leu	Glu	Cys	Val	Asn	Gly	Asp	115	120	125	
Leu	Lys	Ser	Val	Pro	Met	Ile	Ser	Asn	Asn	Val	Thr	Leu	Leu	Ser	Leu	130	135	140	
Lys	Lys	Asn	Lys	Ile	His	Ser	Leu	Pro	Asp	Lys	Val	Phe	Ile	Lys	Tyr	145	150	155	160
Thr	Lys	Leu	Lys	Lys	Ile	Phe	Leu	Gln	His	Asn	Cys	Ile	Arg	His	Ile	165	170	175	
Ser	Arg	Lys	Ala	Phe	Phe	Gly	Leu	Cys	Asn	Leu	Gln	Ile	Leu	Tyr	Leu	180	185	190	
Asn	His	Asn	Cys	Ile	Thr	Thr	Leu	Arg	Pro	Gly	Ile	Phe	Lys	Asp	Leu	195	200	205	
His	Gln	Leu	Thr	Trp	Leu	Ile	Leu	Asp	Asp	Asn	Pro	Ile	Thr	Arg	Ile	210	215	220	
Ser	Gln	Arg	Leu	Phe	Thr	Gly	Leu	Asn	Ser	Leu	Phe	Phe	Leu	Ser	Met	225	230	235	240
Val	Asn	Asn	Tyr	Leu	Glu	Ala	Leu	Pro	Lys	Gln	Met	Cys	Ala	Gln	Met	245	250	255	
Pro	Gln	Leu	Asn	Trp	Val	Asp	Leu	Glu	Gly	Asn	Arg	Ile	Lys	Tyr	Leu	260	265	270	

Thr	Asn	Ser	Thr	Phe	Leu	Ser	Cys	Asp	Ser	Leu	Thr	Val	Leu	Phe	Leu		
	275						280					285					
Pro	Arg	Asn	Gln	Ile	Gly	Phe	Val	Pro	Glu	Lys	Thr	Phe	Ser	Ser	Leu		
	290					295					300						
Lys	Asn	Leu	Gly	Glu	Leu	Asp	Leu	Ser	Ser	Asn	Thr	Ile	Thr	Glu	Leu		
305					310					315					320		
Ser	Pro	His	Leu	Phe	Lys	Asp	Leu	Lys	Leu	Leu	Gln	Lys	Leu	Asn	Leu		
			325						330					335			
Ser	Ser	Asn	Pro	Leu	Met	Tyr	Leu	His	Lys	Asn	Gln	Phe	Glu	Ser	Leu		
		340						345					350				
Lys	Gln	Leu	Gln	Ser	Leu	Asp	Leu	Glu	Arg	Ile	Glu	Ile	Pro	Asn	Ile		
	355						360					365					
Asn	Thr	Arg	Met	Phe	Gln	Pro	Met	Lys	Asn	Leu	Ser	His	Ile	Tyr	Phe		
	370					375					380						
Lys	Asn	Phe	Arg	Tyr	Cys	Ser	Tyr	Ala	Pro	His	Val	Arg	Ile	Cys	Met		
385					390					395					400		
Pro	Leu	Thr	Asp	Gly	Ile	Ser	Ser	Phe	Glu	Asp	Leu	Leu	Ala	Asn	Asn		
				405					410					415			
Ile	Leu	Arg	Ile	Phe	Val	Trp	Val	Ile	Ala	Phe	Ile	Thr	Cys	Phe	Gly		
		420						425					430				
Asn	Leu	Phe	Val	Ile	Gly	Met	Arg	Ser	Phe	Ile	Lys	Ala	Glu	Asn	Thr		
	435					440						445					
Thr	His	Ala	Met	Ser	Ile	Lys	Ile	Leu	Cys	Cys	Ala	Asp	Cys	Leu	Met		
	450					455					460						
Gly	Val	Tyr	Leu	Phe	Phe	Val	Gly	Ile	Phe	Asp	Ile	Lys	Tyr	Arg	Gly		
465					470					475					480		
Gln	Tyr	Gln	Lys	Tyr	Ala	Leu	Leu	Trp	Met	Glu	Ser	Val	Gln	Cys	Arg		
			485						490					495			
Leu	Met	Gly	Phe	Leu	Ala	Met	Leu	Ser	Thr	Glu	Val	Ser	Val	Leu	Leu		
		500						505					510				
Leu	Thr	Tyr	Leu	Thr	Leu	Glu	Lys	Phe	Leu	Val	Ile	Val	Phe	Pro	Phe		
	515						520					525					
Ser	Asn	Ile	Arg	Pro	Gly	Lys	Arg	Gln	Thr	Ser	Val	Ile	Leu	Ile	Cys		
	530					535					540						
Ile	Trp	Met	Ala	Gly	Phe	Leu	Ile	Ala	Val	Ile	Pro	Phe	Trp	Asn	Lys		
545					550				555					560			
Asp	Tyr	Phe	Gly	Asn	Phe	Tyr	Gly	Lys	Asn	Gly	Val	Cys	Phe	Pro	Leu		
			565						570					575			

Tyr Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser Leu Gly
 580 585 590
 Ile Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Ile Ile Val Phe Ser
 595 600 605
 Tyr Ile Thr Met Phe Cys Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr
 610 615 620
 Glu Val Arg Asn Cys Phe Gly Arg Glu Val Ala Val Ala Asn Arg Phe
 625 630 635 640
 Phe Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val
 645 650 655
 Val Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro Asp Thr Met Thr
 660 665 670
 Ser Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro
 675 680 685
 Ile Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln
 690 695 700
 Leu Leu His Lys His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys
 705 710 715 720
 Ser Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu Lys
 725 730 735
 Leu Gly Val Leu Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro
 740 745 750
 Val Ser

<210> 3

<211> 718

<212> PRT

<213> Homo sapiens

<400> 3

Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr Phe Pro Cys
 1 5 10 15

Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys Asp Gly Lys
 20 25 30

Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly Asp Thr Ser
 35 40 45

Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val
 50 55 60

Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln Cys Cys Asp
 65 70 75 80

Cys	Lys	Glu	Thr	Glu	Leu	Glu	Cys	Val	Asn	Gly	Asp	Leu	Lys	Ser	Val	85	90	95
Pro	Met	Ile	Ser	Asn	Asn	Val	Thr	Leu	Leu	Ser	Leu	Lys	Lys	Asn	Lys	100	105	110
Ile	His	Ser	Leu	Pro	Asp	Lys	Val	Phe	Ile	Lys	Tyr	Thr	Lys	Leu	Lys	115	120	125
Lys	Ile	Phe	Leu	Gln	His	Asn	Cys	Ile	Arg	His	Ile	Ser	Arg	Lys	Ala	130	135	140
Phe	Phe	Gly	Leu	Cys	Asn	Leu	Gln	Ile	Leu	Tyr	Leu	Asn	His	Asn	Cys	145	150	155
Ile	Thr	Thr	Leu	Arg	Pro	Gly	Ile	Phe	Lys	Asp	Leu	His	Gln	Leu	Thr	165	170	175
Trp	Leu	Ile	Leu	Asp	Asp	Asn	Pro	Ile	Thr	Arg	Ile	Ser	Gln	Arg	Leu	180	185	190
Phe	Thr	Gly	Leu	Asn	Ser	Leu	Phe	Phe	Leu	Ser	Met	Val	Asn	Asn	Tyr	195	200	205
Leu	Glu	Ala	Leu	Pro	Lys	Gln	Met	Cys	Ala	Gln	Met	Pro	Gln	Leu	Asn	210	215	220
Trp	Val	Asp	Leu	Glu	Gly	Asn	Arg	Ile	Lys	Tyr	Leu	Thr	Asn	Ser	Thr	225	230	235
Phe	Leu	Ser	Cys	Asp	Ser	Leu	Thr	Val	Leu	Phe	Leu	Pro	Arg	Asn	Gln	245	250	255
Ile	Gly	Phe	Val	Pro	Glu	Lys	Thr	Phe	Ser	Ser	Leu	Lys	Asn	Leu	Gly	260	265	270
Glu	Leu	Asp	Leu	Ser	Ser	Asn	Thr	Ile	Thr	Glu	Leu	Ser	Pro	His	Leu	275	280	285
Phe	Lys	Asp	Leu	Lys	Leu	Leu	Gln	Lys	Leu	Asn	Leu	Ser	Ser	Asn	Pro	290	295	300
Leu	Met	Tyr	Leu	His	Lys	Asn	Gln	Phe	Glu	Ser	Leu	Lys	Gln	Leu	Gln	305	310	315
Ser	Leu	Asp	Leu	Glu	Arg	Ile	Glu	Ile	Pro	Asn	Ile	Asn	Thr	Arg	Met	325	330	335
Phe	Gln	Pro	Met	Lys	Asn	Leu	Ser	His	Ile	Tyr	Phe	Lys	Asn	Phe	Arg	340	345	350
Tyr	Cys	Ser	Tyr	Ala	Pro	His	Val	Arg	Ile	Cys	Met	Pro	Leu	Thr	Asp	355	360	365
Gly	Ile	Ser	Ser	Phe	Glu	Asp	Leu	Leu	Ala	Asn	Asn	Ile	Leu	Arg	Ile	370	375	380

Phe Val Trp Val Ile Ala Phe Ile Thr Cys Phe Gly Asn Leu Phe Val
 385 390 395 400
 Ile Gly Met Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr His Ala Met
 405 410 415
 Ser Ile Lys Ile Leu Cys Cys Ala Asp Cys Leu Met Gly Val Tyr Leu
 420 425 430
 Phe Phe Val Gly Ile Phe Asp Ile Lys Tyr Arg Gly Gln Tyr Gln Lys
 435 440 445
 Tyr Ala Leu Leu Trp Met Glu Ser Val Gln Cys Arg Leu Met Gly Phe
 450 455 460
 Leu Ala Met Leu Ser Thr Glu Val Ser Val Leu Leu Leu Thr Tyr Leu
 465 470 475 480
 Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser Asn Ile Arg
 485 490 495
 Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile Cys Ile Trp Met Ala
 500 505 510
 Gly Phe Leu Ile Ala Val Ile Pro Phe Trp Asn Lys Asp Tyr Phe Gly
 515 520 525
 Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu Tyr Tyr Asp Gln
 530 535 540
 Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser Leu Gly Ile Phe Leu Gly
 545 550 555 560
 Val Asn Leu Leu Ala Phe Leu Ile Ile Val Phe Ser Tyr Ile Thr Met
 565 570 575
 Phe Cys Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr Glu Val Arg Asn
 580 585 590
 Cys Phe Gly Arg Glu Val Ala Val Ala Asn Arg Phe Phe Phe Ile Val
 595 600 605
 Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val Val Lys Ile Leu
 610 615 620
 Ser Leu Phe Arg Val Glu Ile Pro Asp Thr Met Thr Ser Trp Ile Val
 625 630 635 640
 Ile Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro Ile Leu Tyr Thr
 645 650 655
 Leu Thr Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln Leu Leu His Lys
 660 665 670
 His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys Ser Leu Ser Thr
 675 680 685

Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu
 690 695 700

Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro Val Ser
 705 710 715

<210> 4
 <211> 1149
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1149)

<400> 4
 caa ggt agc atg atc act cct tca tgc caa aaa gga tat ttt ccc tgt 48
 Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr Phe Pro Cys
 1 5 10 15
 ggg aat ctt acc aag tgc tta ccc cga gct ttt cac tgt gat ggc aag 96
 Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys Asp Gly Lys
 20 25 30
 gat gac tgt ggg aac ggg gcg gac gaa gag aac tgt ggt gac act agt 144
 Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly Asp Thr Ser
 35 40 45
 gga tgg gcg acc ata ttt ggc aca gtg cat gga aat gct aac agc gtg 192
 Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val
 50 55 60
 gcc tta aca cag gag tgc ttt cta aaa cag tat cca caa tgc tgt gac 240
 Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln Cys Cys Asp
 65 70 75 80
 tgc aaa gaa act gaa ttg gaa tgt gta aat ggt gac tta aag tct gtg 288
 Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu Lys Ser Val
 85 90 95
 ccg atg att tct aac aat gtg aca tta ctg tct ctt aag aaa aac aaa 336
 Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys
 100 105 110
 atc cac agt ctt cca gat aaa gtt ttc atc aaa tac aca aaa ctt aaa 384
 Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr Lys Leu Lys
 115 120 125
 aag ata ttt ctt cag cat aat tgc att aga cac ata tcc agg aaa gca 432
 Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser Arg Lys Ala
 130 135 140
 ttt ttt gga tta tgt aat ctg caa ata tta tat ctc aac cac aac tgc 480
 Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn His Asn Cys
 145 150 155 160

atc	aca	acc	ctc	aga	cct	gga	ata	ttc	aaa	gac	tta	cat	cag	cta	act	528
Ile	Thr	Thr	Leu	Arg	Pro	Gly	Ile	Phe	Lys	Asp	Leu	His	Gln	Leu	Thr	
			165						170					175		
tgg	cta	att	cta	gat	gac	aat	cca	ata	acc	aga	att	tca	cag	cgc	ttg	576
Trp	Leu	Ile	Leu	Asp	Asp	Asn	Pro	Ile	Thr	Arg	Ile	Ser	Gln	Arg	Leu	
			180					185					190			
ttt	acg	gga	tta	aat	tcc	ttg	ttt	ttc	ctg	tct	atg	gtt	aat	aac	tac	624
Phe	Thr	Gly	Leu	Asn	Ser	Leu	Phe	Phe	Leu	Ser	Met	Val	Asn	Asn	Tyr	
		195					200					205				
tta	gaa	gct	ctt	ccc	aag	cag	atg	tgt	gcc	caa	atg	cct	caa	ctc	aac	672
Leu	Glu	Ala	Leu	Pro	Lys	Gln	Met	Cys	Ala	Gln	Met	Pro	Gln	Leu	Asn	
	210					215					220					
tgg	gtg	gat	ttg	gaa	ggc	aat	aga	ata	aag	tat	ctc	aca	aat	tct	acg	720
Trp	Val	Asp	Leu	Glu	Gly	Asn	Arg	Ile	Lys	Tyr	Leu	Thr	Asn	Ser	Thr	
225					230					235					240	
ttt	ctg	tcg	tgc	gat	tcg	ctc	aca	gtg	ctg	ttt	ctg	cct	aga	aat	caa	768
Phe	Leu	Ser	Cys	Asp	Ser	Leu	Thr	Val	Leu	Phe	Leu	Pro	Arg	Asn	Gln	
			245						250					255		
att	ggg	ttt	gtt	cca	gag	aag	aca	ttt	tct	tca	tta	aaa	aat	tta	gga	816
Ile	Gly	Phe	Val	Pro	Glu	Lys	Thr	Phe	Ser	Ser	Leu	Lys	Asn	Leu	Gly	
			260					265					270			
gaa	ctg	gat	ctg	tct	agc	aat	acg	ata	acg	gag	cta	tca	cct	cac	ctt	864
Glu	Leu	Asp	Leu	Ser	Ser	Asn	Thr	Ile	Thr	Glu	Leu	Ser	Pro	His	Leu	
		275					280					285				
ttt	aaa	gac	ttg	aag	ctt	cta	caa	aag	ctg	aac	ctg	tca	tcc	aat	cct	912
Phe	Lys	Asp	Leu	Lys	Leu	Leu	Gln	Lys	Leu	Asn	Leu	Ser	Ser	Asn	Pro	
	290					295					300					
ctt	atg	tat	ctt	cac	aag	aac	cag	ttt	gaa	agt	ctt	aaa	caa	ctt	cag	960
Leu	Met	Tyr	Leu	His	Lys	Asn	Gln	Phe	Glu	Ser	Leu	Lys	Gln	Leu	Gln	
305					310					315					320	
tct	cta	gac	ctg	gaa	agg	ata	gag	att	cca	aat	ata	aac	aca	cga	atg	1008
Ser	Leu	Asp	Leu	Glu	Arg	Ile	Glu	Ile	Pro	Asn	Ile	Asn	Thr	Arg	Met	
			325						330					335		
ttt	caa	ccc	atg	aag	aat	ctt	tct	cac	att	tat	ttc	aaa	aac	ttt	cga	1056
Phe	Gln	Pro	Met	Lys	Asn	Leu	Ser	His	Ile	Tyr	Phe	Lys	Asn	Phe	Arg	
		340						345					350			
tac	tgc	tcc	tat	gct	ccc	cat	gtc	cga	ata	tgt	atg	ccc	ttg	acg	gac	1104
Tyr	Cys	Ser	Tyr	Ala	Pro	His	Val	Arg	Ile	Cys	Met	Pro	Leu	Thr	Asp	
		355					360					365				
ggc	att	tct	tca	ttt	gag	gac	ctc	ttg	gct	aac	aat	atc	ctc	aga		1149
Gly	Ile	Ser	Ser	Phe	Glu	Asp	Leu	Leu	Ala	Asn	Asn	Ile	Leu	Arg		
	370					375					380					

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr Phe Pro Cys
1 5 10 15

Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly Asp Thr Ser
35 40 45

Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln Cys Cys Asp
65 70 75 80

Pro	Met	Ile	Ser	Asn	Asn	Val	Thr	Leu	Leu	Ser	Leu	Lys	Lys	Asn	Lys
			100					105					110		

Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser Arg Lys Ala
130 135 140

Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His Gln Leu Thr
165 170 175

Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val Asn Asn Tyr
195 200 205

Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu Thr Asn Ser Thr
225 230 235 240

Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu Lys Asn Leu Gly
260 265 270

Glu Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu
 275 280 285
 Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro
 290 295 300
 Leu Met Tyr Leu His Lys Asn Gln Phe Glu Ser Leu Lys Gln Leu Gln
 305 310 315 320
 Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile Asn Thr Arg Met
 325 330 335
 Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys Asn Phe Arg
 340 345 350
 Tyr Cys Ser Tyr Ala Pro His Val Arg Ile Cys Met Pro Leu Thr Asp
 355 360 365
 Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn Ile Leu Arg
 370 375 380

<210> 6
 <211> 2193
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2190)
 <220>
 <221> sig_peptide
 <222> (1)..(108)

<400> 6
 atg att gtt ttt ctg gtt ttt aaa cat ctc ttc agc ctc aga ttg att 48
 Met Ile Val Phe Leu Val Phe Lys His Leu Phe Ser Leu Arg Leu Ile
 1 5 10 15
 aca atg ttc ttt cta ctt cat ttc atc gtt ctg atc aat gtc aaa gat 96
 Thr Met Phe Phe Leu Leu His Phe Ile Val Leu Ile Asn Val Lys Asp
 20 25 30
 ttt gca ctg act caa ggt agc atg atc act cct tca tgc caa aaa gga 144
 Phe Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly
 35 40 45
 tat ttt ccc tgt ggg aat ctt acc aag tgc tta ccc cga gct ttt cac 192
 Tyr Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His
 50 55 60
 tgt gat ggc aag gat gac tgt ggg aac ggg gcg gac gaa gag aac tgt 240
 Cys Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys
 65 70 75 80

ggt gac act agt gga tgg gcg acc ata ttt ggc aca gtg cat gga aat	288
Gly Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn	
85 90 95	
gct aac agc gtg gcc tta aca cag gag tgc ttt cta aaa cag tat cca	336
Ala Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro	
100 105 110	
caa tgc tgt gac tgc aaa gaa act gaa ttg gaa tgt gta aat ggt gac	384
Gln Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp	
115 120 125	
tta aag tct gtg ccg atg att tct aac aat gtg aca tta ctg tct ctt	432
Leu Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu	
130 135 140	
aag aaa aac aaa atc cac agt ctt cca gat aaa gtt ttc atc aaa tac	480
Lys Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr	
145 150 155 160	
aca aaa ctt aaa aag ata ttt ctt cag cat aat tgc att aga cac ata	528
Thr Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile	
165 170 175	
tcc agg aaa gca ttt ttt gga tta tgt aat ctg caa ata tta tat ctc	576
Ser Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu	
180 185 190	
aac cac aac tgc atc aca acc ctc aga cct gga ata ttc aaa gac tta	624
Asn His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu	
195 200 205	
cat cag cta act tgg cta att cta gat gac aat cca ata acc aga att	672
His Gln Leu Thr Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile	
210 215 220	
tca cag cgc ttg ttt acg gga tta aat tcc ttg ttt ttc ctg tct atg	720
Ser Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met	
225 230 235 240	
gtt aat aac tac tta gaa gct ctt ccc aag cag atg tgt gcc caa atg	768
Val Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met	
245 250 255	
cct caa ctc aac tgg gtg gat ttg gaa ggc aat aga ata aag tat ctc	816
Pro Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu	
260 265 270	
aca aat tct acg ttt ctg tcg tgc gat tcg ctc aca gtg ctg gat ctg	864
Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Asp Leu	
275 280 285	
tct agc aat acg ata acg gag cta tca cct cac ctt ttt aaa gac ttg	912
Ser Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu Phe Lys Asp Leu	
290 295 300	
aag ctt cta caa aag ctg aac ctg tca tcc aat cct ctt atg tat ctt	960

Lys	Leu	Leu	Gln	Lys	Leu	Asn	Leu	Ser	Ser	Asn	Pro	Leu	Met	Tyr	Leu	
305					310					315					320	
cac	aag	aac	cag	ttt	gaa	agt	ctt	aaa	caa	ctt	cag	tct	cta	gac	ctg	1008
His	Lys	Asn	Gln	Phe	Glu	Ser	Leu	Lys	Gln	Leu	Gln	Ser	Leu	Asp	Leu	
				325					330					335		
gaa	agg	ata	gag	att	cca	aat	ata	aac	aca	cga	atg	ttt	caa	ccc	atg	1056
Glu	Arg	Ile	Glu	Ile	Pro	Asn	Ile	Asn	Thr	Arg	Met	Phe	Gln	Pro	Met	
			340					345					350			
aag	aat	ctt	tct	cac	att	tat	ttc	aaa	aac	ttt	cga	tac	tgc	tcc	tat	1104
Lys	Asn	Leu	Ser	His	Ile	Tyr	Phe	Lys	Asn	Phe	Arg	Tyr	Cys	Ser	Tyr	
		355					360					365				
gct	ccc	cat	gtc	cga	ata	tgt	atg	ccc	ttg	acg	gac	ggc	att	tct	tca	1152
Ala	Pro	His	Val	Arg	Ile	Cys	Met	Pro	Leu	Thr	Asp	Gly	Ile	Ser	Ser	
	370					375					380					
ttt	gag	gac	ctc	ttg	gct	aac	aat	atc	ctc	aga	ata	ttt	gtc	tgg	gtt	1200
Phe	Glu	Asp	Leu	Leu	Ala	Asn	Asn	Ile	Leu	Arg	Ile	Phe	Val	Trp	Val	
385					390					395				400		
ata	gct	ttc	att	acc	tgc	ttt	gga	aat	ctt	ttt	gtc	att	ggc	atg	aga	1248
Ile	Ala	Phe	Ile	Thr	Cys	Phe	Gly	Asn	Leu	Phe	Val	Ile	Gly	Met	Arg	
				405					410					415		
tct	ttc	att	aaa	gct	gaa	aat	aca	act	cac	gct	atg	tcc	atc	aaa	atc	1296
Ser	Phe	Ile	Lys	Ala	Glu	Asn	Thr	Thr	His	Ala	Met	Ser	Ile	Lys	Ile	
			420					425					430			
ctt	tgt	tgt	gct	gat	tgc	ctg	atg	ggc	gtt	tac	ttg	ttc	ttt	gtt	ggc	1344
Leu	Cys	Cys	Ala	Asp	Cys	Leu	Met	Gly	Val	Tyr	Leu	Phe	Phe	Val	Gly	
		435					440					445				
att	ttc	gat	ata	aaa	tac	cga	ggg	cag	tat	cag	aag	tat	gcc	ttg	ctg	1392
Ile	Phe	Asp	Ile	Lys	Tyr	Arg	Gly	Gln	Tyr	Gln	Lys	Tyr	Ala	Leu	Leu	
	450					455					460					
tgg	atg	gag	agc	gtg	cag	tgc	cgc	ctc	atg	ggg	ttc	ctg	gcc	atg	ctg	1440
Trp	Met	Glu	Ser	Val	Gln	Cys	Arg	Leu	Met	Gly	Phe	Leu	Ala	Met	Leu	
465					470					475				480		
tcc	acc	gaa	gtc	tct	gtt	ctg	cta	ctg	acc	tac	ttg	act	ttg	gag	aag	1488
Ser	Thr	Glu	Val	Ser	Val	Leu	Leu	Leu	Thr	Tyr	Leu	Thr	Leu	Glu	Lys	
				485					490					495		
ttc	ctg	gtc	att	gtc	ttc	ccc	ttc	agt	aac	att	cga	cct	gga	aaa	cgg	1536
Phe	Leu	Val	Ile	Val	Phe	Pro	Phe	Ser	Asn	Ile	Arg	Pro	Gly	Lys	Arg	
			500					505					510			
cag	acc	tca	gtc	atc	ctc	att	tgc	atc	tgg	atg	gcg	gga	ttt	tta	ata	1584
Gln	Thr	Ser	Val	Ile	Leu	Ile	Cys	Ile	Trp	Met	Ala	Gly	Phe	Leu	Ile	
		515					520					525				
gct	gta	att	cca	ttt	tgg	aat	aag	gat	tat	ttt	gga	aac	ttt	tat	ggg	1632
Ala	Val	Ile	Pro	Phe	Trp	Asn	Lys	Asp	Tyr	Phe	Gly	Asn	Phe	Tyr	Gly	

530	535	540	
aaa aat gga gta tgt ttc cca ctt tat tat gac caa aca gaa gat att			1680
Lys Asn Gly Val Cys Phe Pro Leu Tyr Tyr Asp Gln Thr Glu Asp Ile			
545	550	555	560
gga agc aaa ggg tat tct ctt gga att ttc cta ggt gtg aac ttg ctg			1728
Gly Ser Lys Gly Tyr Ser Leu Gly Ile Phe Leu Gly Val Asn Leu Leu			
	565	570	575
gct ttt ctc atc att gtg ttt tcc tat att act atg ttc tgt tcc att			1776
Ala Phe Leu Ile Ile Val Phe Ser Tyr Ile Thr Met Phe Cys Ser Ile			
	580	585	590
caa aaa acc gcc ttg cag acc aca gaa gta agg aat tgt ttt gga aga			1824
Gln Lys Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe Gly Arg			
	595	600	605
gag gtg gct gtt gca aat cgt ttc ttt ttt ata gtg ttc tct gat gcc			1872
Glu Val Ala Val Ala Asn Arg Phe Phe Phe Ile Val Phe Ser Asp Ala			
	610	615	620
atc tgc tgg att cct gta ttt gta gtt aaa atc ctt tcc ctc ttc cgg			1920
Ile Cys Trp Ile Pro Val Phe Val Val Lys Ile Leu Ser Leu Phe Arg			
	625	630	640
gtg gaa ata cca gac aca atg act tcc tgg ata gtg att ttt ttc ctt			1968
Val Glu Ile Pro Asp Thr Met Thr Ser Trp Ile Val Ile Phe Phe Leu			
	645	650	655
cca gtt aac agt gct ttg aat cca atc ctc tat act ctc aca acc aac			2016
Pro Val Asn Ser Ala Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Asn			
	660	665	670
ttt ttt aag gac aag ttg aaa cag ctg ctg cac aaa cat cag agg aaa			2064
Phe Phe Lys Asp Lys Leu Lys Gln Leu Leu His Lys His Gln Arg Lys			
	675	680	685
tca att ttc aaa att aaa aaa aaa agt tta tct aca tcc att gtg tgg			2112
Ser Ile Phe Lys Ile Lys Lys Lys Ser Leu Ser Thr Ser Ile Val Trp			
	690	695	700
ata gag gac tcc tct tcc ctg aaa ctt ggg gtt ttg aac aaa ata aca			2160
Ile Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn Lys Ile Thr			
	705	710	715
ctt gga gac agt ata atg aaa cca gtt tcc tag			2193
Leu Gly Asp Ser Ile Met Lys Pro Val Ser			
	725	730	

<210> 7

<211> 730

<212> PRT

<213> Homo sapiens

<400> 7

Met	Ile	Val	Phe	Leu	Val	Phe	Lys	His	Leu	Phe	Ser	Leu	Arg	Leu	Ile	1	5	10	15
Thr	Met	Phe	Phe	Leu	Leu	His	Phe	Ile	Val	Leu	Ile	Asn	Val	Lys	Asp	20	25	30	
Phe	Ala	Leu	Thr	Gln	Gly	Ser	Met	Ile	Thr	Pro	Ser	Cys	Gln	Lys	Gly	35	40	45	
Tyr	Phe	Pro	Cys	Gly	Asn	Leu	Thr	Lys	Cys	Leu	Pro	Arg	Ala	Phe	His	50	55	60	
Cys	Asp	Gly	Lys	Asp	Asp	Cys	Gly	Asn	Gly	Ala	Asp	Glu	Glu	Asn	Cys	65	70	75	80
Gly	Asp	Thr	Ser	Gly	Trp	Ala	Thr	Ile	Phe	Gly	Thr	Val	His	Gly	Asn	85	90	95	
Ala	Asn	Ser	Val	Ala	Leu	Thr	Gln	Glu	Cys	Phe	Leu	Lys	Gln	Tyr	Pro	100	105	110	
Gln	Cys	Cys	Asp	Cys	Lys	Glu	Thr	Glu	Leu	Glu	Cys	Val	Asn	Gly	Asp	115	120	125	
Leu	Lys	Ser	Val	Pro	Met	Ile	Ser	Asn	Asn	Val	Thr	Leu	Leu	Ser	Leu	130	135	140	
Lys	Lys	Asn	Lys	Ile	His	Ser	Leu	Pro	Asp	Lys	Val	Phe	Ile	Lys	Tyr	145	150	155	160
Thr	Lys	Leu	Lys	Lys	Ile	Phe	Leu	Gln	His	Asn	Cys	Ile	Arg	His	Ile	165	170	175	
Ser	Arg	Lys	Ala	Phe	Phe	Gly	Leu	Cys	Asn	Leu	Gln	Ile	Leu	Tyr	Leu	180	185	190	
Asn	His	Asn	Cys	Ile	Thr	Thr	Leu	Arg	Pro	Gly	Ile	Phe	Lys	Asp	Leu	195	200	205	
His	Gln	Leu	Thr	Trp	Leu	Ile	Leu	Asp	Asp	Asn	Pro	Ile	Thr	Arg	Ile	210	215	220	
Ser	Gln	Arg	Leu	Phe	Thr	Gly	Leu	Asn	Ser	Leu	Phe	Phe	Leu	Ser	Met	225	230	235	240
Val	Asn	Asn	Tyr	Leu	Glu	Ala	Leu	Pro	Lys	Gln	Met	Cys	Ala	Gln	Met	245	250	255	
Pro	Gln	Leu	Asn	Trp	Val	Asp	Leu	Glu	Gly	Asn	Arg	Ile	Lys	Tyr	Leu	260	265	270	
Thr	Asn	Ser	Thr	Phe	Leu	Ser	Cys	Asp	Ser	Leu	Thr	Val	Leu	Asp	Leu	275	280	285	
Ser	Ser	Asn	Thr	Ile	Thr	Glu	Leu	Ser	Pro	His	Leu	Phe	Lys	Asp	Leu	290	295	300	

Lys Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr Leu
 305 310 315 320
 His Lys Asn Gln Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu Asp Leu
 325 330 335
 Glu Arg Ile Glu Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met
 340 345 350
 Lys Asn Leu Ser His Ile Tyr Phe Lys Asn Phe Arg Tyr Cys Ser Tyr
 355 360 365
 Ala Pro His Val Arg Ile Cys Met Pro Leu Thr Asp Gly Ile Ser Ser
 370 375 380
 Phe Glu Asp Leu Leu Ala Asn Asn Ile Leu Arg Ile Phe Val Trp Val
 385 390 395 400
 Ile Ala Phe Ile Thr Cys Phe Gly Asn Leu Phe Val Ile Gly Met Arg
 405 410 415
 Ser Phe Ile Lys Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys Ile
 420 425 430
 Leu Cys Cys Ala Asp Cys Leu Met Gly Val Tyr Leu Phe Phe Val Gly
 435 440 445
 Ile Phe Asp Ile Lys Tyr Arg Gly Gln Tyr Gln Lys Tyr Ala Leu Leu
 450 455 460
 Trp Met Glu Ser Val Gln Cys Arg Leu Met Gly Phe Leu Ala Met Leu
 465 470 475 480
 Ser Thr Glu Val Ser Val Leu Leu Leu Thr Tyr Leu Thr Leu Glu Lys
 485 490 495
 Phe Leu Val Ile Val Phe Pro Phe Ser Asn Ile Arg Pro Gly Lys Arg
 500 505 510
 Gln Thr Ser Val Ile Leu Ile Cys Ile Trp Met Ala Gly Phe Leu Ile
 515 520 525
 Ala Val Ile Pro Phe Trp Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly
 530 535 540
 Lys Asn Gly Val Cys Phe Pro Leu Tyr Tyr Asp Gln Thr Glu Asp Ile
 545 550 555 560
 Gly Ser Lys Gly Tyr Ser Leu Gly Ile Phe Leu Gly Val Asn Leu Leu
 565 570 575
 Ala Phe Leu Ile Ile Val Phe Ser Tyr Ile Thr Met Phe Cys Ser Ile
 580 585 590
 Gln Lys Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe Gly Arg
 595 600 605

Glu Val Ala Val Ala Asn Arg Phe Phe Phe Ile Val Phe Ser Asp Ala
 610 615 620

Ile Cys Trp Ile Pro Val Phe Val Val Lys Ile Leu Ser Leu Phe Arg
 625 630 635 640

Val Glu Ile Pro Asp Thr Met Thr Ser Trp Ile Val Ile Phe Phe Leu
 645 650 655

Pro Val Asn Ser Ala Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Asn
 660 665 670

Phe Phe Lys Asp Lys Leu Lys Gln Leu Leu His Lys His Gln Arg Lys
 675 680 685

Ser Ile Phe Lys Ile Lys Lys Lys Ser Leu Ser Thr Ser Ile Val Trp
 690 695 700

Ile Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn Lys Ile Thr
 705 710 715 720

Leu Gly Asp Ser Ile Met Lys Pro Val Ser
 725 730

<210> 8

<211> 694

<212> PRT

<213> Homo sapiens

<400> 8

Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr Phe Pro Cys
 1 5 10 15

Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys Asp Gly Lys
 20 25 30

Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly Asp Thr Ser
 35 40 45

Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val
 50 55 60

Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln Cys Cys Asp
 65 70 75 80

Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu Lys Ser Val
 85 90 95

Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys
 100 105 110

Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr Lys Leu Lys
 115 120 125

Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser Arg Lys Ala
 130 135 140

Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn His Asn Cys
145 150 155 160
Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His Gln Leu Thr
165 170 175
Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile Ser Gln Arg Leu
180 185 190
Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val Asn Asn Tyr
195 200 205
Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met Pro Gln Leu Asn
210 215 220
Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu Thr Asn Ser Thr
225 230 235 240
Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Asp Leu Ser Ser Asn Thr
245 250 255
Ile Thr Glu Leu Ser Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln
260 265 270
Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln
275 280 285
Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu
290 295 300
Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser
305 310 315 320
His Ile Tyr Phe Lys Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val
325 330 335
Arg Ile Cys Met Pro Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu
340 345 350
Leu Ala Asn Asn Ile Leu Arg Ile Phe Val Trp Val Ile Ala Phe Ile
355 360 365
Thr Cys Phe Gly Asn Leu Phe Val Ile Gly Met Arg Ser Phe Ile Lys
370 375 380
Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala
385 390 395 400
Asp Cys Leu Met Gly Val Tyr Leu Phe Phe Val Gly Ile Phe Asp Ile
405 410 415
Lys Tyr Arg Gly Gln Tyr Gln Lys Tyr Ala Leu Leu Trp Met Glu Ser
420 425 430
Val Gln Cys Arg Leu Met Gly Phe Leu Ala Met Leu Ser Thr Glu Val
435 440 445

Ser Val Leu Leu Leu Thr Tyr Leu Thr Leu Glu Lys Phe Leu Val Ile
 450 455 460
 Val Phe Pro Phe Ser Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val
 465 470 475 480
 Ile Leu Ile Cys Ile Trp Met Ala Gly Phe Leu Ile Ala Val Ile Pro
 485 490 495
 Phe Trp Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val
 500 505 510
 Cys Phe Pro Leu Tyr Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly
 515 520 525
 Tyr Ser Leu Gly Ile Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Ile
 530 535 540
 Ile Val Phe Ser Tyr Ile Thr Met Phe Cys Ser Ile Gln Lys Thr Ala
 545 550 555 560
 Leu Gln Thr Thr Glu Val Arg Asn Cys Phe Gly Arg Glu Val Ala Val
 565 570 575
 Ala Asn Arg Phe Phe Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile
 580 585 590
 Pro Val Phe Val Val Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro
 595 600 605
 Asp Thr Met Thr Ser Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser
 610 615 620
 Ala Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp
 625 630 635 640
 Lys Leu Lys Gln Leu Leu His Lys His Gln Arg Lys Ser Ile Phe Lys
 645 650 655
 Ile Lys Lys Lys Ser Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser
 660 665 670
 Ser Ser Leu Lys Leu Gly Val Leu Asn Lys Ile Thr Leu Gly Asp Ser
 675 680 685
 Ile Met Lys Pro Val Ser
 690

<210> 9
 <211> 1077
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (1)..(1077)

<400> 9

caa ggt agc atg atc act cct tca tgc caa aaa gga tat ttt ccc tgt	48
Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr Phe Pro Cys	
1 5 10 15	
ggg aat ctt acc aag tgc tta ccc cga gct ttt cac tgt gat ggc aag	96
Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys Asp Gly Lys	
20 25 30	
gat gac tgt ggg aac ggg gcg gac gaa gag aac tgt ggt gac act agt	144
Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly Asp Thr Ser	
35 40 45	
gga tgg gcg acc ata ttt ggc aca gtg cat gga aat gct aac agc gtg	192
Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val	
50 55 60	
gcc tta aca cag gag tgc ttt cta aaa cag tat cca caa tgc tgt gac	240
Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln Cys Cys Asp	
65 70 75 80	
tgc aaa gaa act gaa ttg gaa tgt gta aat ggt gac tta aag tct gtg	288
Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu Lys Ser Val	
85 90 95	
ccg atg att tct aac aat gtg aca tta ctg tct ctt aag aaa aac aaa	336
Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys	
100 105 110	
atc cac agt ctt cca gat aaa gtt ttc atc aaa tac aca aaa ctt aaa	384
Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr Lys Leu Lys	
115 120 125	
aag ata ttt ctt cag cat aat tgc att aga cac ata tcc agg aaa gca	432
Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser Arg Lys Ala	
130 135 140	
ttt ttt gga tta tgt aat ctg caa ata tta tat ctc aac cac aac tgc	480
Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn His Asn Cys	
145 150 155 160	
atc aca acc ctc aga cct gga ata ttc aaa gac tta cat cag cta act	528
Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His Gln Leu Thr	
165 170 175	
tgg cta att cta gat gac aat cca ata acc aga att tca cag cgc ttg	576
Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile Ser Gln Arg Leu	
180 185 190	
ttt acg gga tta aat tcc ttg ttt ttc ctg tct atg gtt aat aac tac	624
Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val Asn Asn Tyr	
195 200 205	
tta gaa gct ctt ccc aag cag atg tgt gcc caa atg cct caa ctc aac	672
Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met Pro Gln Leu Asn	

Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln Cys Cys Asp
 65 70 75 80
 Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu Lys Ser Val
 85 90 95
 Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys
 100 105 110
 Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr Lys Leu Lys
 115 120 125
 Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser Arg Lys Ala
 130 135 140
 Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn His Asn Cys
 145 150 155 160
 Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His Gln Leu Thr
 165 170 175
 Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile Ser Gln Arg Leu
 180 185 190
 Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val Asn Asn Tyr
 195 200 205
 Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met Pro Gln Leu Asn
 210 215 220
 Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu Thr Asn Ser Thr
 225 230 235 240
 Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Asp Leu Ser Ser Asn Thr
 245 250 255
 Ile Thr Glu Leu Ser Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln
 260 265 270
 Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln
 275 280 285
 Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu
 290 295 300
 Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser
 305 310 315 320
 His Ile Tyr Phe Lys Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val
 325 330 335
 Arg Ile Cys Met Pro Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu
 340 345 350
 Leu Ala Asn Asn Ile Leu Arg
 355

<210> 11
 <211> 2049
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2046)

<220>
 <221> sig_peptide
 <222> (1)..(108)

<400> 11

atg att gtt ttt ctg gtt ttt aaa cat ctc ttc agc ctc aga ttg att	48
Met Ile Val Phe Leu Val Phe Lys His Leu Phe Ser Leu Arg Leu Ile	
1 5 10 15	
aca atg ttc ttt cta ctt cat ttc atc gtt ctg atc aat gtc aaa gat	96
Thr Met Phe Phe Leu Leu His Phe Ile Val Leu Ile Asn Val Lys Asp	
20 25 30	
ttt gca ctg act caa ggt agc atg atc act cct tca tgc caa aaa gga	144
Phe Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly	
35 40 45	
tat ttt ccc tgt ggg aat ctt acc aag tgc tta ccc cga gct ttt cac	192
Tyr Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His	
50 55 60	
tgt gat ggc aag gat gac tgt ggg aac ggg gcg gac gaa gag aac tgt	240
Cys Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys	
65 70 75 80	
ggg gac act agt gga tgg gcg acc ata ttt ggc aca gtg cat gga aat	288
Gly Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn	
85 90 95	
gct aac agc gtg gcc tta aca cag gag tgc ttt cta aaa cag tat cca	336
Ala Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro	
100 105 110	
caa tgc tgt gac tgc aaa gaa act gaa ttg gaa tgt gta aat ggt gac	384
Gln Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp	
115 120 125	
tta aag tct gtg ccg atg att tct aac aat gtg aca tta ctg tct ctt	432
Leu Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu	
130 135 140	
aag aaa aac aaa atc cac agt ctt cca gat aaa gtt ttc atc aaa tac	480
Lys Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr	
145 150 155 160	
aca aaa ctt aaa aag ata ttt ctt cag cat aat tgc att aga cac ata	528
Thr Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile	

																165																	170																	175																
tcc	agg	aaa	gca	ttt	ttt	gga	tta	tgt	aat	ctg	caa	ata	tta	att	cta	576																																																		
Ser	Arg	Lys	Ala	Phe	Phe	Gly	Leu	Cys	Asn	Leu	Gln	Ile	Leu	Ile	Leu																																																			
			180							185							190																																																	
gat	gac	aat	cca	ata	acc	aga	att	tca	cag	cgc	ttg	ttt	acg	gga	tta	624																																																		
Asp	Asp	Asn	Pro	Ile	Thr	Arg	Ile	Ser	Gln	Arg	Leu	Phe	Thr	Gly	Leu																																																			
			195							200							205																																																	
aat	tcc	ttg	ttt	ttc	ctg	tct	atg	gtt	aat	aac	tac	tta	gaa	gct	ctt	672																																																		
Asn	Ser	Leu	Phe	Phe	Leu	Ser	Met	Val	Asn	Asn	Tyr	Leu	Glu	Ala	Leu																																																			
			210							215							220																																																	
ccc	aag	cag	atg	tgt	gcc	caa	atg	cct	caa	ctc	aac	tgg	gtg	gat	ttg	720																																																		
Pro	Lys	Gln	Met	Cys	Ala	Gln	Met	Pro	Gln	Leu	Asn	Trp	Val	Asp	Leu																																																			
225																240																																																		
gaa	ggc	aat	aga	ata	aag	tat	ctc	aca	aat	tct	acg	ttt	ctg	tcg	tgc	768																																																		
Glu	Gly	Asn	Arg	Ile	Lys	Tyr	Leu	Thr	Asn	Ser	Thr	Phe	Leu	Ser	Cys																																																			
																		255																																																
gat	tcg	ctc	aca	gtg	ctg	gat	ctg	tct	agc	aat	acg	ata	acg	gag	cta	816																																																		
Asp	Ser	Leu	Thr	Val	Leu	Asp	Leu	Ser	Ser	Asn	Thr	Ile	Thr	Glu	Leu																																																			
																		270																																																
tca	cct	cac	ctt	ttt	aaa	gac	ttg	aag	ctt	cta	caa	aag	cta	gac	ctg	864																																																		
Ser	Pro	His	Leu	Phe	Lys	Asp	Leu	Lys	Leu	Leu	Gln	Lys	Leu	Asp	Leu																																																			
																		285																																																
gaa	agg	ata	gag	att	cca	aat	ata	aac	aca	cga	atg	ttt	caa	ccc	atg	912																																																		
Glu	Arg	Ile	Glu	Ile	Pro	Asn	Ile	Asn	Thr	Arg	Met	Phe	Gln	Pro	Met																																																			
																		300																																																
aag	aat	ctt	tct	cac	att	tat	ttc	aaa	aac	ttt	cga	tac	tgc	tcc	tat	960																																																		
Lys	Asn	Leu	Ser	His	Ile	Tyr	Phe	Lys	Asn	Phe	Arg	Tyr	Cys	Ser	Tyr																																																			
305																			320																																															
gct	ccc	cat	gtc	cga	ata	tgt	atg	ccc	ttg	acg	gac	ggc	att	tct	tca	1008																																																		
Ala	Pro	His	Val	Arg	Ile	Cys	Met	Pro	Leu	Thr	Asp	Gly	Ile	Ser	Ser																																																			
																		335																																																
ttt	gag	gac	ctc	ttg	gct	aac	aat	atc	ctc	aga	ata	ttt	gtc	tgg	gtt	1056																																																		
Phe	Glu	Asp	Leu	Leu	Ala	Asn	Asn	Ile	Leu	Arg	Ile	Phe	Val	Trp	Val																																																			
																		350																																																
ata	gct	ttc	att	acc	tgc	ttt	gga	aat	ctt	ttt	gtc	att	ggc	atg	aga	1104																																																		
Ile	Ala	Phe	Ile	Thr	Cys	Phe	Gly	Asn	Leu	Phe	Val	Ile	Gly	Met	Arg																																																			
																		365																																																
tct	ttc	att	aaa	gct	gaa	aat	aca	act	cac	gct	atg	tcc	atc	aaa	atc																																																			

att ttc gat ata aaa tac cga ggg cag tat cag aag tat gcc ttg ctg	1248
Ile Phe Asp Ile Lys Tyr Arg Gly Gln Tyr Gln Lys Tyr Ala Leu Leu	
405 410 415	
tgg atg gag agc gtg cag tgc cgc ctc atg ggg ttc ctg gcc atg ctg	1296
Trp Met Glu Ser Val Gln Cys Arg Leu Met Gly Phe Leu Ala Met Leu	
420 425 430	
tcc acc gaa gtc tct gtt ctg cta ctg acc tac ttg act ttg gag aag	1344
Ser Thr Glu Val Ser Val Leu Leu Leu Thr Tyr Leu Thr Leu Glu Lys	
435 440 445	
ttc ctg gtc att gtc ttc ccc ttc agt aac att cga cct gga aaa cgg	1392
Phe Leu Val Ile Val Phe Pro Phe Ser Asn Ile Arg Pro Gly Lys Arg	
450 455 460	
cag acc tca gtc atc ctc att tgc atc tgg atg gcg gga ttt tta ata	1440
Gln Thr Ser Val Ile Leu Ile Cys Ile Trp Met Ala Gly Phe Leu Ile	
465 470 475 480	
gct gta att cca ttt tgg aat aag gat tat ttt gga aac ttt tat ggg	1488
Ala Val Ile Pro Phe Trp Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly	
485 490 495	
aaa aat gga gta tgt ttc cca ctt tat tat gac caa aca gaa gat att	1536
Lys Asn Gly Val Cys Phe Pro Leu Tyr Tyr Asp Gln Thr Glu Asp Ile	
500 505 510	
gga agc aaa ggg tat tct ctt gga att ttc cta ggt gtg aac ttg ctg	1584
Gly Ser Lys Gly Tyr Ser Leu Gly Ile Phe Leu Gly Val Asn Leu Leu	
515 520 525	
gct ttt ctc atc att gtg ttt tcc tat att act atg ttc tgt tcc att	1632
Ala Phe Leu Ile Ile Val Phe Ser Tyr Ile Thr Met Phe Cys Ser Ile	
530 535 540	
caa aaa acc gcc ttg cag acc aca gaa gta agg aat tgt ttt gga aga	1680
Gln Lys Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe Gly Arg	
545 550 555 560	
gag gtg gct gtt gca aat cgt ttc ttt ttt ata gtg ttc tct gat gcc	1728
Glu Val Ala Val Ala Asn Arg Phe Phe Phe Ile Val Phe Ser Asp Ala	
565 570 575	
atc tgc tgg att cct gta ttt gta gtt aaa atc ctt tcc ctc ttc cgg	1776
Ile Cys Trp Ile Pro Val Phe Val Val Lys Ile Leu Ser Leu Phe Arg	
580 585 590	
gtg gaa ata cca gac aca atg act tcc tgg ata gtg att ttt ttc ctt	1824
Val Glu Ile Pro Asp Thr Met Thr Ser Trp Ile Val Ile Phe Phe Leu	
595 600 605	
cca gtt aac agt gct ttg aat cca atc ctc tat act ctc aca acc aac	1872
Pro Val Asn Ser Ala Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Asn	
610 615 620	

180	185	190
Asp Asp Asn Pro Ile Thr Arg Ile Ser Gln Arg Leu Phe Thr Gly Leu 195 200 205		
Asn Ser Leu Phe Phe Leu Ser Met Val Asn Asn Tyr Leu Glu Ala Leu 210 215 220		
Pro Lys Gln Met Cys Ala Gln Met Pro Gln Leu Asn Trp Val Asp Leu 225 230 235 240		
Glu Gly Asn Arg Ile Lys Tyr Leu Thr Asn Ser Thr Phe Leu Ser Cys 245 250 255		
Asp Ser Leu Thr Val Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu 260 265 270		
Ser Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asp Leu 275 280 285		
Glu Arg Ile Glu Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met 290 295 300		
Lys Asn Leu Ser His Ile Tyr Phe Lys Asn Phe Arg Tyr Cys Ser Tyr 305 310 315 320		
Ala Pro His Val Arg Ile Cys Met Pro Leu Thr Asp Gly Ile Ser Ser 325 330 335		
Phe Glu Asp Leu Leu Ala Asn Asn Ile Leu Arg Ile Phe Val Trp Val 340 345 350		
Ile Ala Phe Ile Thr Cys Phe Gly Asn Leu Phe Val Ile Gly Met Arg 355 360 365		
Ser Phe Ile Lys Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys Ile 370 375 380		
Leu Cys Cys Ala Asp Cys Leu Met Gly Val Tyr Leu Phe Phe Val Gly 385 390 395 400		
Ile Phe Asp Ile Lys Tyr Arg Gly Gln Tyr Gln Lys Tyr Ala Leu Leu 405 410 415		
Trp Met Glu Ser Val Gln Cys Arg Leu Met Gly Phe Leu Ala Met Leu 420 425 430		
Ser Thr Glu Val Ser Val Leu Leu Leu Thr Tyr Leu Thr Leu Glu Lys 435 440 445		
Phe Leu Val Ile Val Phe Pro Phe Ser Asn Ile Arg Pro Gly Lys Arg 450 455 460		
Gln Thr Ser Val Ile Leu Ile Cys Ile Trp Met Ala Gly Phe Leu Ile 465 470 475 480		
Ala Val Ile Pro Phe Trp Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly		

485	490	495
Lys Asn Gly Val Cys Phe Pro Leu Tyr Tyr Asp Gln Thr Glu Asp Ile		
500	505	510
Gly Ser Lys Gly Tyr Ser Leu Gly Ile Phe Leu Gly Val Asn Leu Leu		
515	520	525
Ala Phe Leu Ile Ile Val Phe Ser Tyr Ile Thr Met Phe Cys Ser Ile		
530	535	540
Gln Lys Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe Gly Arg		
545	550	555
Glu Val Ala Val Ala Asn Arg Phe Phe Phe Ile Val Phe Ser Asp Ala		
565	570	575
Ile Cys Trp Ile Pro Val Phe Val Val Lys Ile Leu Ser Leu Phe Arg		
580	585	590
Val Glu Ile Pro Asp Thr Met Thr Ser Trp Ile Val Ile Phe Phe Leu		
595	600	605
Pro Val Asn Ser Ala Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Asn		
610	615	620
Phe Phe Lys Asp Lys Leu Lys Gln Leu Leu His Lys His Gln Arg Lys		
625	630	635
Ser Ile Phe Lys Ile Lys Lys Lys Ser Leu Ser Thr Ser Ile Val Trp		
645	650	655
Ile Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn Lys Ile Thr		
660	665	670
Leu Gly Asp Ser Ile Met Lys Pro Val Ser		
675	680	

<210> 13

<211> 646

<212> PRT

<213> Homo sapiens

<400> 13

Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr Phe Pro Cys
1 5 10 15
Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys Asp Gly Lys
20 25 30
Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly Asp Thr Ser
35 40 45
Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val
50 55 60

Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln Cys Cys Asp
 65 70 75 80
 Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu Lys Ser Val
 85 90 95
 Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys
 100 105 110
 Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr Lys Leu Lys
 115 120 125
 Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser Arg Lys Ala
 130 135 140
 Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Ile Leu Asp Asp Asn Pro
 145 150 155 160
 Ile Thr Arg Ile Ser Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe
 165 170 175
 Phe Leu Ser Met Val Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met
 180 185 190
 Cys Ala Gln Met Pro Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg
 195 200 205
 Ile Lys Tyr Leu Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr
 210 215 220
 Val Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu
 225 230 235 240
 Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asp Leu Glu Arg Ile Glu
 245 250 255
 Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser
 260 265 270
 His Ile Tyr Phe Lys Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val
 275 280 285
 Arg Ile Cys Met Pro Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu
 290 295 300
 Leu Ala Asn Asn Ile Leu Arg Ile Phe Val Trp Val Ile Ala Phe Ile
 305 310 315 320
 Thr Cys Phe Gly Asn Leu Phe Val Ile Gly Met Arg Ser Phe Ile Lys
 325 330 335
 Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala
 340 345 350
 Asp Cys Leu Met Gly Val Tyr Leu Phe Phe Val Gly Ile Phe Asp Ile
 355 360 365

Lys Tyr Arg Gly Gln Tyr Gln Lys Tyr Ala Leu Leu Trp Met Glu Ser
 370 375 380
 Val Gln Cys Arg Leu Met Gly Phe Leu Ala Met Leu Ser Thr Glu Val
 385 390 395 400
 Ser Val Leu Leu Leu Thr Tyr Leu Thr Leu Glu Lys Phe Leu Val Ile
 405 410 415
 Val Phe Pro Phe Ser Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val
 420 425 430
 Ile Leu Ile Cys Ile Trp Met Ala Gly Phe Leu Ile Ala Val Ile Pro
 435 440 445
 Phe Trp Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val
 450 455 460
 Cys Phe Pro Leu Tyr Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly
 465 470 475 480
 Tyr Ser Leu Gly Ile Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Ile
 485 490 495
 Ile Val Phe Ser Tyr Ile Thr Met Phe Cys Ser Ile Gln Lys Thr Ala
 500 505 510
 Leu Gln Thr Thr Glu Val Arg Asn Cys Phe Gly Arg Glu Val Ala Val
 515 520 525
 Ala Asn Arg Phe Phe Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile
 530 535 540
 Pro Val Phe Val Val Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro
 545 550 555 560
 Asp Thr Met Thr Ser Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser
 565 570 575
 Ala Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp
 580 585 590
 Lys Leu Lys Gln Leu Leu His Lys His Gln Arg Lys Ser Ile Phe Lys
 595 600 605
 Ile Lys Lys Lys Ser Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser
 610 615 620
 Ser Ser Leu Lys Leu Gly Val Leu Asn Lys Ile Thr Leu Gly Asp Ser
 625 630 635 640
 Ile Met Lys Pro Val Ser
 645

<210> 14

<211> 933

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(933)

<400> 14

caa ggt agc atg atc act cct tca tgc caa aaa gga tat ttt ccc tgt	48
Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr Phe Pro Cys	
1 5 10 15	
ggg aat ctt acc aag tgc tta ccc cga gct ttt cac tgt gat ggc aag	96
Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys Asp Gly Lys	
20 25 30	
gat gac tgt ggg aac ggg gcg gac gaa gag aac tgt ggt gac act agt	144
Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly Asp Thr Ser	
35 40 45	
gga tgg gcg acc ata ttt ggc aca gtg cat gga aat gct aac agc gtg	192
Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val	
50 55 60	
gcc tta aca cag gag tgc ttt cta aaa cag tat cca caa tgc tgt gac	240
Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln Cys Cys Asp	
65 70 75 80	
tgc aaa gaa act gaa ttg gaa tgt gta aat ggt gac tta aag tct gtg	288
Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu Lys Ser Val	
85 90 95	
ccg atg att tct aac aat gtg aca tta ctg tct ctt aag aaa aac aaa	336
Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys	
100 105 110	
atc cac agt ctt cca gat aaa gtt ttc atc aaa tac aca aaa ctt aaa	384
Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr Lys Leu Lys	
115 120 125	
aag ata ttt ctt cag cat aat tgc att aga cac ata tcc agg aaa gca	432
Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser Arg Lys Ala	
130 135 140	
ttt ttt gga tta tgt aat ctg caa ata tta att cta gat gac aat cca	480
Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Ile Leu Asp Asp Asn Pro	
145 150 155 160	
ata acc aga att tca cag cgc ttg ttt acg gga tta aat tcc ttg ttt	528
Ile Thr Arg Ile Ser Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe	
165 170 175	
ttc ctg tct atg gtt aat aac tac tta gaa gct ctt ccc aag cag atg	576
Phe Leu Ser Met Val Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met	
180 185 190	
tgt gcc caa atg cct caa ctc aac tgg gtg gat ttg gaa ggc aat aga	624

Cys Ala Gln Met Pro Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg
 195 200 205

ata aag tat ctc aca aat tct acg ttt ctg tgc gat tgc ctc aca 672
 Ile Lys Tyr Leu Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr
 210 215 220

gtg ctg gat ctg tct agc aat acg ata acg gag cta tca cct cac ctt 720
 Val Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu
 225 230 235 240

ttt aaa gac ttg aag ctt cta caa aag cta gac ctg gaa agg ata gag 768
 Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asp Leu Glu Arg Ile Glu
 245 250 255

att cca aat ata aac aca cga atg ttt caa ccc atg aag aat ctt tct 816
 Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser
 260 265 270

cac att tat ttc aaa aac ttt cga tac tgc tcc tat gct ccc cat gtc 864
 His Ile Tyr Phe Lys Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val
 275 280 285

cga ata tgt atg ccc ttg acg gac ggc att tct tca ttt gag gac ctc 912
 Arg Ile Cys Met Pro Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu
 290 295 300

ttg gct aac aat atc ctc aga 933
 Leu Ala Asn Asn Ile Leu Arg
 305 310

<210> 15
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 15
 Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr Phe Pro Cys
 1 5 10 15

Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys Asp Gly Lys
 20 25 30

Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly Asp Thr Ser
 35 40 45

Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val
 50 55 60

Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln Cys Cys Asp
 65 70 75 80

Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu Lys Ser Val
 85 90 95

Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys

100	105	110
Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr Lys Leu Lys 115 120 125		
Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser Arg Lys Ala 130 135 140		
Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Ile Leu Asp Asp Asn Pro 145 150 155 160		
Ile Thr Arg Ile Ser Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe 165 170 175		
Phe Leu Ser Met Val Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met 180 185 190		
Cys Ala Gln Met Pro Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg 195 200 205		
Ile Lys Tyr Leu Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr 210 215 220		
Val Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu 225 230 235 240		
Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asp Leu Glu Arg Ile Glu 245 250 255		
Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser 260 265 270		
His Ile Tyr Phe Lys Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val 275 280 285		
Arg Ile Cys Met Pro Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu 290 295 300		
Leu Ala Asn Asn Ile Leu Arg 305 310		

<210> 16
 <211> 1101
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1098)

<220>
 <221> sig_peptide
 <222> (1)..(108)

<400> 16
 atg att gtt ttt ctg gtt ttt aaa cat ctc ttc agc ctc aga ttg att 48

Met	Ile	Val	Phe	Leu	Val	Phe	Lys	His	Leu	Phe	Ser	Leu	Arg	Leu	Ile		
1				5					10					15			
aca	atg	ttc	ttt	cta	ctt	cat	ttc	atc	gtt	ctg	atc	aat	gtc	aaa	gat	96	
Thr	Met	Phe	Phe	Leu	Leu	His	Phe	Ile	Val	Leu	Ile	Asn	Val	Lys	Asp		
			20					25					30				
ttt	gca	ctg	act	caa	ggg	agc	atg	atc	act	cct	tca	tgc	caa	aaa	gga	144	
Phe	Ala	Leu	Thr	Gln	Gly	Ser	Met	Ile	Thr	Pro	Ser	Cys	Gln	Lys	Gly		
		35					40					45					
tat	ttt	ccc	tgt	ggg	aat	ctt	acc	aag	tgc	tta	ccc	cga	gct	ttt	cac	192	
Tyr	Phe	Pro	Cys	Gly	Asn	Leu	Thr	Lys	Cys	Leu	Pro	Arg	Ala	Phe	His		
	50					55					60						
tgt	gat	ggc	aag	gat	gac	tgt	ggg	aac	ggg	gcg	gac	gaa	gag	aac	tgt	240	
Cys	Asp	Gly	Lys	Asp	Asp	Cys	Gly	Asn	Gly	Ala	Asp	Glu	Glu	Asn	Cys		
	65				70				75					80			
ggg	gac	act	agt	gga	tgg	gag	acc	ata	ttt	ggc	aca	gtg	cat	gga	aat	288	
Gly	Asp	Thr	Ser	Gly	Trp	Ala	Thr	Ile	Phe	Gly	Thr	Val	His	Gly	Asn		
				85				90					95				
gct	aac	agc	gtg	gcc	tta	aca	cag	gag	tgc	ttt	cta	aaa	cag	tat	cca	336	
Ala	Asn	Ser	Val	Ala	Leu	Thr	Gln	Glu	Cys	Phe	Leu	Lys	Gln	Tyr	Pro		
			100				105						110				
caa	tgc	tgt	gac	tgc	aaa	gaa	act	gaa	ttg	gaa	tgt	gta	aat	ggg	gac	384	
Gln	Cys	Cys	Asp	Cys	Lys	Glu	Thr	Glu	Leu	Glu	Cys	Val	Asn	Gly	Asp		
		115				120						125					
tta	aag	tct	gtg	ccg	atg	att	tct	aac	aat	gtg	aca	tta	ctg	tct	ctt	432	
Leu	Lys	Ser	Val	Pro	Met	Ile	Ser	Asn	Asn	Val	Thr	Leu	Leu	Ser	Leu		
	130					135					140						
aag	aaa	aac	aaa	atc	cac	agt	ctt	cca	gat	aaa	gtt	ttc	atc	aaa	tac	480	
Lys	Lys	Asn	Lys	Ile	His	Ser	Leu	Pro	Asp	Lys	Val	Phe	Ile	Lys	Tyr		
	145				150				155					160			
aca	aaa	ctt	aaa	aag	ata	ttt	ctt	cag	cat	aat	tgc	att	aga	cac	ata	528	
Thr	Lys	Leu	Lys	Lys	Ile	Phe	Leu	Gln	His	Asn	Cys	Ile	Arg	His	Ile		
			165					170					175				
tcc	agg	aaa	gca	ttt	ttt	gga	tta	tgt	aat	ctg	caa	ata	tta	tat	ctc	576	
Ser	Arg	Lys	Ala	Phe	Phe	Gly	Leu	Cys	Asn	Leu	Gln	Ile	Leu	Tyr	Leu		
			180				185						190				
aac	cac	aac	tgc	atc	aca	acc	ctc	aga	cct	gga	ata	ttc	aaa	gac	tta	624	
Asn	His	Asn	Cys	Ile	Thr	Thr	Leu	Arg	Pro	Gly	Ile	Phe	Lys	Asp	Leu		
		195					200				205						
cat	cag	cta	act	tgg	cta	att	cta	gat	gac	aat	cca	ata	acc	aga	att	672	
His	Gln	Leu	Thr	Trp	Leu	Ile	Leu	Asp	Asp	Asn	Pro	Ile	Thr	Arg	Ile		
	210				215					220							
tca	cag	cgc	ttg	ttt	acg	gga	tta	aat	tcc	ttg	ttt	ttc	ctg	tct	atg	720	
Ser	Gln	Arg	Leu	Phe	Thr	Gly	Leu	Asn	Ser	Leu	Phe	Phe	Leu	Ser	Met		

225	230	235	240	
gtt aat aac tac tta gaa gct ctt ccc aag cag atg tgt gcc caa atg				768
Val Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met	245	250	255	
cct caa ctc aac tgg gtg gat ttg gaa ggc aat aga ata aag tat ctc				816
Pro Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu	260	265	270	
aca aat tct acg ttt ctg tcg tgc gat tcg ctc aca gtg ctg gat ctg				864
Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Asp Leu	275	280	285	
tct agc aat acg ata acg gag cta tca cct cac ctt ttt aaa gac ttg				912
Ser Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu Phe Lys Asp Leu	290	295	300	
aag ctt cta caa aag ctg aac ctg tca tcc aat cct ctt atg tat ctt				960
Lys Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr Leu	305	310	315	320
cac aag aac cag ttt gaa agt ctt aaa caa ctt cag tct cta gac ctg				1008
His Lys Asn Gln Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu Asp Leu	325	330	335	
gaa agg ata gag att cca aat ata aac aca cga atg ttt caa ccc atg				1056
Glu Arg Ile Glu Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met	340	345	350	
aag aat ctt tct cac ata gtt caa tat tat gat gtg ccg aca tga				1101
Lys Asn Leu Ser His Ile Val Gln Tyr Tyr Asp Val Pro Thr	355	360	365	

<210> 17

<211> 366

<212> PRT

<213> Homo sapiens

<400> 17

Met Ile Val Phe Leu Val Phe Lys His Leu Phe Ser Leu Arg Leu Ile			
1	5	10	15
Thr Met Phe Phe Leu Leu His Phe Ile Val Leu Ile Asn Val Lys Asp			
20	25	30	
Phe Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly			
35	40	45	
Tyr Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His			
50	55	60	
Cys Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys			
65	70	75	80
Gly Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn			

85

90

95

Ala Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro
 100 105 110

Gln Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp
 115 120 125

Leu Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu
 130 135 140

Lys Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr
 145 150 155 160

Thr Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile
 165 170 175

Ser Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu
 180 185 190

Asn His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu
 195 200 205

His Gln Leu Thr Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile
 210 215 220

Ser Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met
 225 230 235 240

Val Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met
 245 250 255

Pro Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu
 260 265 270

Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Asp Leu
 275 280 285

Ser Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu Phe Lys Asp Leu
 290 295 300

Lys Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr Leu
 305 310 315 320

His Lys Asn Gln Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu Asp Leu
 325 330 335

Glu Arg Ile Glu Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met
 340 345 350

Lys Asn Leu Ser His Ile Val Gln Tyr Tyr Asp Val Pro Thr
 355 360 365

<210> 18

<211> 330

<212> PRT

<213> Homo sapiens

<400> 18

Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr Phe Pro Cys
1 5 10 15

Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys Asp Gly Lys
20 25 30

Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly Asp Thr Ser
35 40 45

Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val
50 55 60

Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln Cys Cys Asp
65 70 75 80

Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu Lys Ser Val
85 90 95

Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys
100 105 110

Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr Lys Leu Lys
115 120 125

Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser Arg Lys Ala
130 135 140

Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn His Asn Cys
145 150 155 160

Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His Gln Leu Thr
165 170 175

Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile Ser Gln Arg Leu
180 185 190

Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val Asn Asn Tyr
195 200 205

Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met Pro Gln Leu Asn
210 215 220

Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu Thr Asn Ser Thr
225 230 235 240

Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Asp Leu Ser Ser Asn Thr
245 250 255

Ile Thr Glu Leu Ser Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln
260 265 270

Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln
275 280 285

Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu
 290 295 300

Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser
 305 310 315 320

His Ile Val Gln Tyr Tyr Asp Val Pro Thr
 325 330

<210> 19

<211> 2214

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(2211)

<220>

<221> sig_peptide

<222> (1)..(57)

<400> 19

atg tgg ctc cta ctt cat gtc atc ctt ctg aca gag gtc aaa gat ttt 48
 Met Trp Leu Leu Leu His Val Ile Leu Leu Thr Glu Val Lys Asp Phe
 1 5 10 15

gca ctg gct gac agc agt atg gtg gct cct ctg tgc ccc aaa ggg tat 96
 Ala Leu Ala Asp Ser Ser Met Val Ala Pro Leu Cys Pro Lys Gly Tyr
 20 25 30

ttt ccc tgt ggg aat ctc acc aaa tgc ttg ccc cga gcc ttt cac tgc 144
 Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
 35 40 45

gat ggt gtg gat gat tgc ggg aat ggt gcc gac gag gac aac tgt ggt 192
 Asp Gly Val Asp Asp Cys Gly Asn Gly Ala Asp Glu Asp Asn Cys Gly
 50 55 60

gac act agt gga tgg aca acc ata ttt ggc aca gtc cat ggg aat gtc 240
 Asp Thr Ser Gly Trp Thr Thr Ile Phe Gly Thr Val His Gly Asn Val
 65 70 75 80

aat aaa gtg aca ttg aca cag gag tgc ttt ctc agc cag tat cca cag 288
 Asn Lys Val Thr Leu Thr Gln Glu Cys Phe Leu Ser Gln Tyr Pro Gln
 85 90 95

cac tgt tac tgc aga gaa aat gaa ctg gaa tgt gta aag gct gac tta 336
 His Cys Tyr Cys Arg Glu Asn Glu Leu Glu Cys Val Lys Ala Asp Leu
 100 105 110

aaa gct gtg cca aag gtt tcc agc aac gta aca tta cta tct ctt aag 384
 Lys Ala Val Pro Lys Val Ser Ser Asn Val Thr Leu Leu Ser Leu Lys
 115 120 125

aaa aac aaa atc cac aga ctt cca gtc aag gtc ttc agc aga tac aca 432

Lys	Asn	Lys	Ile	His	Arg	Leu	Pro	Val	Lys	Val	Phe	Ser	Arg	Tyr	Thr		
130						135					140						
gaa	ctc	aga	aag	ata	tac	ctt	cag	cac	aac	tgc	atc	aca	cac	atc	tcc	480	
Glu	Leu	Arg	Lys	Ile	Tyr	Leu	Gln	His	Asn	Cys	Ile	Thr	His	Ile	Ser		
145					150					155					160		
agg	aga	gca	ttc	ctt	gga	tta	cat	aat	cta	caa	ata	ctg	tat	ctc	agc	528	
Arg	Arg	Ala	Phe	Leu	Gly	Leu	His	Asn	Leu	Gln	Ile	Leu	Tyr	Leu	Ser		
				165					170					175			
cat	aac	tgc	att	acc	tct	ctc	agg	cct	ggg	ata	ttc	aaa	gac	ttg	cat	576	
His	Asn	Cys	Ile	Thr	Ser	Leu	Arg	Pro	Gly	Ile	Phe	Lys	Asp	Leu	His		
			180					185					190				
cag	ctt	gct	tgg	cta	att	tta	gat	gac	aac	ccg	atc	acc	aga	atc	tca	624	
Gln	Leu	Ala	Trp	Leu	Ile	Leu	Asp	Asp	Asn	Pro	Ile	Thr	Arg	Ile	Ser		
		195					200					205					
cag	aag	tcc	ttt	atg	ggg	tta	aac	tcc	ttg	ttt	ttc	ttg	tcc	atg	gtg	672	
Gln	Lys	Ser	Phe	Met	Gly	Leu	Asn	Ser	Leu	Phe	Phe	Leu	Ser	Met	Val		
	210					215					220						
ggg	aac	cgg	ctc	gag	gcc	ctt	cct	gaa	aca	ttg	tgt	gct	cag	atg	cct	720	
Gly	Asn	Arg	Leu	Glu	Ala	Leu	Pro	Glu	Thr	Leu	Cys	Ala	Gln	Met	Pro		
225					230					235					240		
caa	ctc	aac	tgg	gtg	gat	ctg	gca	aac	aat	gga	ata	aag	tac	ata	acg	768	
Gln	Leu	Asn	Trp	Val	Asp	Leu	Ala	Asn	Asn	Gly	Ile	Lys	Tyr	Ile	Thr		
				245					250					255			
aac	tcc	acc	ttc	cta	acg	tgc	gac	tcg	ctc	acg	ggt	ctg	ttt	ctg	cct	816	
Asn	Ser	Thr	Phe	Leu	Thr	Cys	Asp	Ser	Leu	Thr	Val	Leu	Phe	Leu	Pro		
			260					265					270				
aga	aat	caa	att	ggg	ttt	gtt	cca	gag	aag	aca	ttt	tct	tca	tta	aaa	864	
Arg	Asn	Gln	Ile	Gly	Phe	Val	Pro	Glu	Lys	Thr	Phe	Ser	Ser	Leu	Lys		
		275					280					285					
aat	tta	gga	gaa	ctg	gac	ctg	tct	agc	aat	atg	ata	aca	aaa	ctc	cca	912	
Asn	Leu	Gly	Glu	Leu	Asp	Leu	Ser	Ser	Asn	Met	Ile	Thr	Lys	Leu	Pro		
	290					295					300						
gtc	cac	ctt	ttc	agc	gac	ctt	cat	ctt	ctc	cag	aag	ctg	aac	ctg	tca	960	
Val	His	Leu	Phe	Ser	Asp	Leu	His	Leu	Leu	Gln	Lys	Leu	Asn	Leu	Ser		
305					310					315					320		
tcc	aac	cct	ctt	ctg	tat	gtc	cac	aag	aac	cag	ttt	gga	agt	ctc	aaa	1008	
Ser	Asn	Pro	Leu	Leu	Tyr	Val	His	Lys	Asn	Gln	Phe	Gly	Ser	Leu	Lys		
			325						330					335			
caa	ctt	cag	tct	cta	gac	ctg	gaa	agg	ata	gag	att	cca	aac	ata	agc	1056	
Gln	Leu	Gln	Ser	Leu	Asp	Leu	Glu	Arg	Ile	Glu	Ile	Pro	Asn	Ile	Ser		
			340					345					350				
aca	gga	atg	ttc	cag	cca	atg	aag	aac	ctt	tct	cac	att	tat	ttg	aaa	1104	
Thr	Gly	Met	Phe	Gln	Pro	Met	Lys	Asn	Leu	Ser	His	Ile	Tyr	Leu	Lys		

355		360		365	
acc ttt cga tac tgc tcc tat gtc ccc cat gtc cga atc tgt atg ccg	1152				
Thr Phe Arg Tyr Cys Ser Tyr Val Pro His Val Arg Ile Cys Met Pro					
370		375		380	
tcg act gat ggt att tct tct gtc tct gag gac ctc ttg gct aac ggt atc	1200				
Ser Thr Asp Gly Ile Ser Ser Ser Glu Asp Leu Leu Ala Asn Gly Ile					
385		390		395	400
ctc aga gtg tct gtc tgg gtt ata gct ttc att acc tgc gtt ggg aat	1248				
Leu Arg Val Ser Val Trp Val Ile Ala Phe Ile Thr Cys Val Gly Asn					
		405		410	415
ttc ctt gtc ata gcc gtg aga tct ctc att aag gct gag aat aca act	1296				
Phe Leu Val Ile Ala Val Arg Ser Leu Ile Lys Ala Glu Asn Thr Thr					
		420		425	430
cac gct atg tcc atc aaa atc ctt tgt tgt gcc gat tgc ctg atg ggg	1344				
His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala Asp Cys Leu Met Gly					
		435		440	445
gtg tac ctg ttc tcc gtg ggc gtc ttt gac atc aag tac cga ggg cag	1392				
Val Tyr Leu Phe Ser Val Gly Val Phe Asp Ile Lys Tyr Arg Gly Gln					
		450		455	460
tat cag aag tat gcg ctg ctg tgg atg gag agt gtg ccc tgc cgc ctg	1440				
Tyr Gln Lys Tyr Ala Leu Leu Trp Met Glu Ser Val Pro Cys Arg Leu					
		465		470	475
ctg ggc ttc ctg gcc acg ctg tcc aca gag gtc tgc gtg ctg ctg ctg	1488				
Leu Gly Phe Leu Ala Thr Leu Ser Thr Glu Val Ser Val Leu Leu Leu					
		485		490	495
aca ttc ctg acg ctg gag aag ttc ctt gtc ata gta ttc cct ttc agc	1536				
Thr Phe Leu Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser					
		500		505	510
aac ctg cgc ctg ggc aag cgc cag act gct gtg gcc ctc gcc agc atc	1584				
Asn Leu Arg Leu Gly Lys Arg Gln Thr Ala Val Ala Leu Ala Ser Ile					
		515		520	525
tgg gtg gtg gga ttt ctc ata gcg gcc gtt ccg ttc acc aga gag gat	1632				
Trp Val Val Gly Phe Leu Ile Ala Ala Val Pro Phe Thr Arg Glu Asp					
		530		535	540
tat ttc ggc aac ttt tat ggg aaa aat gga gtc tgc ttc cca ctt cat	1680				
Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu His					
		545		550	555
tat gac caa gca gaa gat ttt gga agt aga ggg tac tcc ctt ggg att	1728				
Tyr Asp Gln Ala Glu Asp Phe Gly Ser Arg Gly Tyr Ser Leu Gly Ile					
		565		570	575
ttc cta ggt gtg aac ttg ctg gct ttc ctc gtc atc gtg att tcc tat	1776				
Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Val Ile Val Ile Ser Tyr					
		580		585	590

gtc acc atg ttc tgc tcc att cat aaa aca gcc ctt cag act gca gaa 1824
 Val Thr Met Phe Cys Ser Ile His Lys Thr Ala Leu Gln Thr Ala Glu
 595 600 605

gtg agg agc cac atc ggg aag gag gtg gct gtt gca aac cgg ttc ttt 1872
 Val Arg Ser His Ile Gly Lys Glu Val Ala Val Ala Asn Arg Phe Phe
 610 615 620

ttt atc gtg ttc tct gat gcc atc tgc tgg atc cct gtg ttt gtc gtt 1920
 Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val Val
 625 630 635 640

aag atc ctg tct ctc ctt caa gtg gag ata cca ggc aca atc act tcc 1968
 Lys Ile Leu Ser Leu Leu Gln Val Glu Ile Pro Gly Thr Ile Thr Ser
 645 650 655

tgg atc gtg gtt ttt ttc ctt ccg gtg aac agc gcc tta aac ccc atc 2016
 Trp Ile Val Val Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro Ile
 660 665 670

ctc tac act ctg acg acc tcc ttt ttt aag gac aag ttg aaa cag ttg 2064
 Leu Tyr Thr Leu Thr Thr Ser Phe Phe Lys Asp Lys Leu Lys Gln Leu
 675 680 685

ctg cac aaa cat cgg agg aaa ccc atc ttc aaa gtt aag aag aaa agt 2112
 Leu His Lys His Arg Arg Lys Pro Ile Phe Lys Val Lys Lys Lys Ser
 690 695 700

tta tcc gct tcc att gtg tgg aca gac gag tct tca ctt aaa ctt gga 2160
 Leu Ser Ala Ser Ile Val Trp Thr Asp Glu Ser Ser Leu Lys Leu Gly
 705 710 715 720

gtg ttg agc aaa ata gcc ctt ggg gac agt ata atg aag ccg gtc tcc 2208
 Val Leu Ser Lys Ile Ala Leu Gly Asp Ser Ile Met Lys Pro Val Ser
 725 730 735

ccg tag 2214
 Pro

<210> 20

<211> 737

<212> PRT

<213> Mus musculus

<400> 20

Met Trp Leu Leu Leu His Val Ile Leu Leu Thr Glu Val Lys Asp Phe
 1 5 10 15

Ala Leu Ala Asp Ser Ser Met Val Ala Pro Leu Cys Pro Lys Gly Tyr
 20 25 30

Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
 35 40 45

Asp Gly Val Asp Asp Cys Gly Asn Gly Ala Asp Glu Asp Asn Cys Gly

50

55

60

Asp Thr Ser Gly Trp Thr Thr Ile Phe Gly Thr Val His Gly Asn Val
65 70 75 80

Asn Lys Val Thr Leu Thr Gln Glu Cys Phe Leu Ser Gln Tyr Pro Gln
85 90 95

His Cys Tyr Cys Arg Glu Asn Glu Leu Glu Cys Val Lys Ala Asp Leu
100 105 110

Lys Ala Val Pro Lys Val Ser Ser Asn Val Thr Leu Leu Ser Leu Lys
115 120 125

Lys Asn Lys Ile His Arg Leu Pro Val Lys Val Phe Ser Arg Tyr Thr
130 135 140

Glu Leu Arg Lys Ile Tyr Leu Gln His Asn Cys Ile Thr His Ile Ser
145 150 155 160

Arg Arg Ala Phe Leu Gly Leu His Asn Leu Gln Ile Leu Tyr Leu Ser
165 170 175

His Asn Cys Ile Thr Ser Leu Arg Pro Gly Ile Phe Lys Asp Leu His
180 185 190

Gln Leu Ala Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile Ser
195 200 205

Gln Lys Ser Phe Met Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val
210 215 220

Gly Asn Arg Leu Glu Ala Leu Pro Glu Thr Leu Cys Ala Gln Met Pro
225 230 235 240

Gln Leu Asn Trp Val Asp Leu Ala Asn Asn Gly Ile Lys Tyr Ile Thr
245 250 255

Asn Ser Thr Phe Leu Thr Cys Asp Ser Leu Thr Val Leu Phe Leu Pro
260 265 270

Arg Asn Gln Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu Lys
275 280 285

Asn Leu Gly Glu Leu Asp Leu Ser Ser Asn Met Ile Thr Lys Leu Pro
290 295 300

Val His Leu Phe Ser Asp Leu His Leu Leu Gln Lys Leu Asn Leu Ser
305 310 315 320

Ser Asn Pro Leu Leu Tyr Val His Lys Asn Gln Phe Gly Ser Leu Lys
325 330 335

Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile Ser
340 345 350

Thr Gly Met Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Leu Lys

660	665	670
Leu Tyr Thr Leu Thr Thr Ser Phe Phe Lys Asp Lys Leu Lys Gln Leu		
675	680	685
Leu His Lys His Arg Arg Lys Pro Ile Phe Lys Val Lys Lys Lys Ser		
690	695	700
Leu Ser Ala Ser Ile Val Trp Thr Asp Glu Ser Ser Leu Lys Leu Gly		
705	710	715
Val Leu Ser Lys Ile Ala Leu Gly Asp Ser Ile Met Lys Pro Val Ser		
725	730	735

Pro

<210> 21
 <211> 718
 <212> PRT
 <213> Mus musculus

<400> 21
 Asp Ser Ser Met Val Ala Pro Leu Cys Pro Lys Gly Tyr Phe Pro Cys
 1 5 10 15
 Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys Asp Gly Val
 20 25 30
 Asp Asp Cys Gly Asn Gly Ala Asp Glu Asp Asn Cys Gly Asp Thr Ser
 35 40 45
 Gly Trp Thr Thr Ile Phe Gly Thr Val His Gly Asn Val Asn Lys Val
 50 55 60
 Thr Leu Thr Gln Glu Cys Phe Leu Ser Gln Tyr Pro Gln His Cys Tyr
 65 70 75 80
 Cys Arg Glu Asn Glu Leu Glu Cys Val Lys Ala Asp Leu Lys Ala Val
 85 90 95
 Pro Lys Val Ser Ser Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys
 100 105 110
 Ile His Arg Leu Pro Val Lys Val Phe Ser Arg Tyr Thr Glu Leu Arg
 115 120 125
 Lys Ile Tyr Leu Gln His Asn Cys Ile Thr His Ile Ser Arg Arg Ala
 130 135 140
 Phe Leu Gly Leu His Asn Leu Gln Ile Leu Tyr Leu Ser His Asn Cys
 145 150 155 160
 Ile Thr Ser Leu Arg Pro Gly Ile Phe Lys Asp Leu His Gln Leu Ala
 165 170 175

Trp	Leu	Ile	Leu	Asp	Asp	Asn	Pro	Ile	Thr	Arg	Ile	Ser	Gln	Lys	Ser	
			180					185					190			
Phe	Met	Gly	Leu	Asn	Ser	Leu	Phe	Phe	Leu	Ser	Met	Val	Gly	Asn	Arg	
		195					200					205				
Leu	Glu	Ala	Leu	Pro	Glu	Thr	Leu	Cys	Ala	Gln	Met	Pro	Gln	Leu	Asn	
	210					215					220					
Trp	Val	Asp	Leu	Ala	Asn	Asn	Gly	Ile	Lys	Tyr	Ile	Thr	Asn	Ser	Thr	
225					230					235					240	
Phe	Leu	Thr	Cys	Asp	Ser	Leu	Thr	Val	Leu	Phe	Leu	Pro	Arg	Asn	Gln	
			245						250					255		
Ile	Gly	Phe	Val	Pro	Glu	Lys	Thr	Phe	Ser	Ser	Leu	Lys	Asn	Leu	Gly	
		260						265					270			
Glu	Leu	Asp	Leu	Ser	Ser	Asn	Met	Ile	Thr	Lys	Leu	Pro	Val	His	Leu	
		275					280					285				
Phe	Ser	Asp	Leu	His	Leu	Leu	Gln	Lys	Leu	Asn	Leu	Ser	Ser	Asn	Pro	
	290					295					300					
Leu	Leu	Tyr	Val	His	Lys	Asn	Gln	Phe	Gly	Ser	Leu	Lys	Gln	Leu	Gln	
305					310					315					320	
Ser	Leu	Asp	Leu	Glu	Arg	Ile	Glu	Ile	Pro	Asn	Ile	Ser	Thr	Gly	Met	
				325					330					335		
Phe	Gln	Pro	Met	Lys	Asn	Leu	Ser	His	Ile	Tyr	Leu	Lys	Thr	Phe	Arg	
			340					345					350			
Tyr	Cys	Ser	Tyr	Val	Pro	His	Val	Arg	Ile	Cys	Met	Pro	Ser	Thr	Asp	
		355					360					365				
Gly	Ile	Ser	Ser	Ser	Glu	Asp	Leu	Leu	Ala	Asn	Gly	Ile	Leu	Arg	Val	
	370					375					380					
Ser	Val	Trp	Val	Ile	Ala	Phe	Ile	Thr	Cys	Val	Gly	Asn	Phe	Leu	Val	
385					390					395					400	
Ile	Ala	Val	Arg	Ser	Leu	Ile	Lys	Ala	Glu	Asn	Thr	Thr	His	Ala	Met	
				405					410					415		
Ser	Ile	Lys	Ile	Leu	Cys	Cys	Ala	Asp	Cys	Leu	Met	Gly	Val	Tyr	Leu	
			420					425					430			
Phe	Ser	Val	Gly	Val	Phe	Asp	Ile	Lys	Tyr	Arg	Gly	Gln	Tyr	Gln	Lys	
		435					440					445				
Tyr	Ala	Leu	Leu	Trp	Met	Glu	Ser	Val	Pro	Cys	Arg	Leu	Leu	Gly	Phe	
	450					455					460					
Leu	Ala	Thr	Leu	Ser	Thr	Glu	Val	Ser	Val	Leu	Leu	Leu	Thr	Phe	Leu	
465					470					475					480	

Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser Asn Leu Arg
 485 490 495
 Leu Gly Lys Arg Gln Thr Ala Val Ala Leu Ala Ser Ile Trp Val Val
 500 505 510
 Gly Phe Leu Ile Ala Ala Val Pro Phe Thr Arg Glu Asp Tyr Phe Gly
 515 520 525
 Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu His Tyr Asp Gln
 530 535 540
 Ala Glu Asp Phe Gly Ser Arg Gly Tyr Ser Leu Gly Ile Phe Leu Gly
 545 550 555 560
 Val Asn Leu Leu Ala Phe Leu Val Ile Val Ile Ser Tyr Val Thr Met
 565 570 575
 Phe Cys Ser Ile His Lys Thr Ala Leu Gln Thr Ala Glu Val Arg Ser
 580 585 590
 His Ile Gly Lys Glu Val Ala Val Ala Asn Arg Phe Phe Phe Ile Val
 595 600 605
 Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val Val Lys Ile Leu
 610 615 620
 Ser Leu Leu Gln Val Glu Ile Pro Gly Thr Ile Thr Ser Trp Ile Val
 625 630 635 640
 Val Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro Ile Leu Tyr Thr
 645 650 655
 Leu Thr Thr Ser Phe Phe Lys Asp Lys Leu Lys Gln Leu Leu His Lys
 660 665 670
 His Arg Arg Lys Pro Ile Phe Lys Val Lys Lys Lys Ser Leu Ser Ala
 675 680 685
 Ser Ile Val Trp Thr Asp Glu Ser Ser Leu Lys Leu Gly Val Leu Ser
 690 695 700
 Lys Ile Ala Leu Gly Asp Ser Ile Met Lys Pro Val Ser Pro
 705 710 715

<210> 22

<211> 1140

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1140)

<400> 22

gac agc agt atg gtg gct cct ctg tgc ccc aaa ggg tat ttt ccc tgt 48

Asp	Ser	Ser	Met	Val	Ala	Pro	Leu	Cys	Pro	Lys	Gly	Tyr	Phe	Pro	Cys		
1				5					10					15			
ggg	aat	ctc	acc	aaa	tgc	ttg	ccc	cga	gcc	ttt	cac	tgc	gat	ggg	gtg	96	
Gly	Asn	Leu	Thr	Lys	Cys	Leu	Pro	Arg	Ala	Phe	His	Cys	Asp	Gly	Val		
			20					25					30				
gat	gat	tgc	ggg	aat	ggg	gcc	gac	gag	gac	aac	tgt	ggg	gac	act	agt	144	
Asp	Asp	Cys	Gly	Asn	Gly	Ala	Asp	Glu	Asp	Asn	Cys	Gly	Asp	Thr	Ser		
		35					40					45					
gga	tgg	aca	acc	ata	ttt	ggc	aca	gtc	cat	ggg	aat	gtc	aat	aaa	gtg	192	
Gly	Trp	Thr	Thr	Ile	Phe	Gly	Thr	Val	His	Gly	Asn	Val	Asn	Lys	Val		
	50					55					60						
aca	ttg	aca	cag	gag	tgc	ttt	ctc	agc	cag	tat	cca	cag	cac	tgt	tac	240	
Thr	Leu	Thr	Gln	Glu	Cys	Phe	Leu	Ser	Gln	Tyr	Pro	Gln	His	Cys	Tyr		
	65				70				75					80			
tgc	aga	gaa	aat	gaa	ctg	gaa	tgt	gta	aag	gct	gac	tta	aaa	gct	gtg	288	
Cys	Arg	Glu	Asn	Glu	Leu	Glu	Cys	Val	Lys	Ala	Asp	Leu	Lys	Ala	Val		
				85				90					95				
cca	aag	gtt	tcc	agc	aac	gta	aca	tta	cta	tct	ctt	aag	aaa	aac	aaa	336	
Pro	Lys	Val	Ser	Ser	Asn	Val	Thr	Leu	Leu	Ser	Leu	Lys	Lys	Asn	Lys		
			100					105					110				
atc	cac	aga	ctt	cca	gtc	aag	gtc	ttc	agc	aga	tac	aca	gaa	ctc	aga	384	
Ile	His	Arg	Leu	Pro	Val	Lys	Val	Phe	Ser	Arg	Tyr	Thr	Glu	Leu	Arg		
		115					120					125					
aag	ata	tac	ctt	cag	cac	aac	tgc	atc	aca	cac	atc	tcc	agg	aga	gca	432	
Lys	Ile	Tyr	Leu	Gln	His	Asn	Cys	Ile	Thr	His	Ile	Ser	Arg	Arg	Ala		
	130					135					140						
ttc	ctt	gga	tta	cat	aat	cta	caa	ata	ctg	tat	ctc	agc	cat	aac	tgc	480	
Phe	Leu	Gly	Leu	His	Asn	Leu	Gln	Ile	Leu	Tyr	Leu	Ser	His	Asn	Cys		
	145				150				155					160			
att	acc	tct	ctc	agg	cct	ggg	ata	ttc	aaa	gac	ttg	cat	cag	ctt	gct	528	
Ile	Thr	Ser	Leu	Arg	Pro	Gly	Ile	Phe	Lys	Asp	Leu	His	Gln	Leu	Ala		
			165					170					175				
tgg	cta	att	tta	gat	gac	aac	ccg	atc	acc	aga	atc	tca	cag	aag	tcc	576	
Trp	Leu	Ile	Leu	Asp	Asp	Asn	Pro	Ile	Thr	Arg	Ile	Ser	Gln	Lys	Ser		
			180					185					190				
ttt	atg	ggg	tta	aac	tcc	ttg	ttt	ttc	ttg	tcc	atg	gtg	ggg	aac	cgg	624	
Phe	Met	Gly	Leu	Asn	Ser	Leu	Phe	Phe	Leu	Ser	Met	Val	Gly	Asn	Arg		
	195					200					205						
ctc	gag	gcc	ctt	cct	gaa	aca	ttg	tgt	gct	cag	atg	cct	caa	ctc	aac	672	
Leu	Glu	Ala	Leu	Pro	Glu	Thr	Leu	Cys	Ala	Gln	Met	Pro	Gln	Leu	Asn		
	210					215				220							
tgg	gtg	gat	ctg	gca	aac	aat	gga	ata	aag	tac	ata	acg	aac	tcc	acc	720	
Trp	Val	Asp	Leu	Ala	Asn	Asn	Gly	Ile	Lys	Tyr	Ile	Thr	Asn	Ser	Thr		

225	230	235	240	
ttc cta acg tgc gac tcg ctc acg gtt ctg ttt ctg cct aga aat caa				768
Phe Leu Thr Cys Asp Ser Leu Thr Val Leu Phe Leu Pro Arg Asn Gln				
245		250	255	
att ggt ttt gtt cca gag aag aca ttt tct tca tta aaa aat tta gga				816
Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu Lys Asn Leu Gly				
260	265		270	
gaa ctg gac ctg tct agc aat atg ata aca aaa ctc cca gtc cac ctt				864
Glu Leu Asp Leu Ser Ser Asn Met Ile Thr Lys Leu Pro Val His Leu				
275	280		285	
ttc agc gac ctt cat ctt ctc cag aag ctg aac ctg tca tcc aac cct				912
Phe Ser Asp Leu His Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro				
290	295	300		
ctt ctg tat gtc cac aag aac cag ttt gga agt ctc aaa caa ctt cag				960
Leu Leu Tyr Val His Lys Asn Gln Phe Gly Ser Leu Lys Gln Leu Gln				
305	310	315	320	
tct cta gac ctg gaa agg ata gag att cca aac ata agc aca gga atg				1008
Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile Ser Thr Gly Met				
325	330		335	
ttc cag cca atg aag aac ctt tct cac att tat ttg aaa acc ttt cga				1056
Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Leu Lys Thr Phe Arg				
340	345		350	
tac tgc tcc tat gtc ccc cat gtc cga atc tgt atg ccg tcg act gat				1104
Tyr Cys Ser Tyr Val Pro His Val Arg Ile Cys Met Pro Ser Thr Asp				
355	360		365	
ggt att tct tcg tct gag gac ctc ttg gct aac ggt				1140
Gly Ile Ser Ser Ser Glu Asp Leu Leu Ala Asn Gly				
370	375	380		

<210> 23

<211> 380

<212> PRT

<213> Mus musculus

<400> 23

Asp	Ser	Ser	Met	Val	Ala	Pro	Leu	Cys	Pro	Lys	Gly	Tyr	Phe	Pro	Cys
1				5					10					15	

Gly	Asn	Leu	Thr	Lys	Cys	Leu	Pro	Arg	Ala	Phe	His	Cys	Asp	Gly	Val
		20						25					30		

Asp	Asp	Cys	Gly	Asn	Gly	Ala	Asp	Glu	Asp	Asn	Cys	Gly	Asp	Thr	Ser
		35				40						45			

Gly	Trp	Thr	Thr	Ile	Phe	Gly	Thr	Val	His	Gly	Asn	Val	Asn	Lys	Val
	50					55					60				

Thr	Leu	Thr	Gln	Glu	Cys	Phe	Leu	Ser	Gln	Tyr	Pro	Gln	His	Cys	Tyr	65	70	75	80
Cys	Arg	Glu	Asn	Glu	Leu	Glu	Cys	Val	Lys	Ala	Asp	Leu	Lys	Ala	Val	85	90	95	
Pro	Lys	Val	Ser	Ser	Asn	Val	Thr	Leu	Leu	Ser	Leu	Lys	Lys	Asn	Lys	100	105	110	
Ile	His	Arg	Leu	Pro	Val	Lys	Val	Phe	Ser	Arg	Tyr	Thr	Glu	Leu	Arg	115	120	125	
Lys	Ile	Tyr	Leu	Gln	His	Asn	Cys	Ile	Thr	His	Ile	Ser	Arg	Arg	Ala	130	135	140	
Phe	Leu	Gly	Leu	His	Asn	Leu	Gln	Ile	Leu	Tyr	Leu	Ser	His	Asn	Cys	145	150	155	160
Ile	Thr	Ser	Leu	Arg	Pro	Gly	Ile	Phe	Lys	Asp	Leu	His	Gln	Leu	Ala	165	170	175	
Trp	Leu	Ile	Leu	Asp	Asp	Asn	Pro	Ile	Thr	Arg	Ile	Ser	Gln	Lys	Ser	180	185	190	
Phe	Met	Gly	Leu	Asn	Ser	Leu	Phe	Phe	Leu	Ser	Met	Val	Gly	Asn	Arg	195	200	205	
Leu	Glu	Ala	Leu	Pro	Glu	Thr	Leu	Cys	Ala	Gln	Met	Pro	Gln	Leu	Asn	210	215	220	
Trp	Val	Asp	Leu	Ala	Asn	Asn	Gly	Ile	Lys	Tyr	Ile	Thr	Asn	Ser	Thr	225	230	235	240
Phe	Leu	Thr	Cys	Asp	Ser	Leu	Thr	Val	Leu	Phe	Leu	Pro	Arg	Asn	Gln	245	250	255	
Ile	Gly	Phe	Val	Pro	Glu	Lys	Thr	Phe	Ser	Ser	Leu	Lys	Asn	Leu	Gly	260	265	270	
Glu	Leu	Asp	Leu	Ser	Ser	Asn	Met	Ile	Thr	Lys	Leu	Pro	Val	His	Leu	275	280	285	
Phe	Ser	Asp	Leu	His	Leu	Leu	Gln	Lys	Leu	Asn	Leu	Ser	Ser	Asn	Pro	290	295	300	
Leu	Leu	Tyr	Val	His	Lys	Asn	Gln	Phe	Gly	Ser	Leu	Lys	Gln	Leu	Gln	305	310	315	320
Ser	Leu	Asp	Leu	Glu	Arg	Ile	Glu	Ile	Pro	Asn	Ile	Ser	Thr	Gly	Met	325	330	335	
Phe	Gln	Pro	Met	Lys	Asn	Leu	Ser	His	Ile	Tyr	Leu	Lys	Thr	Phe	Arg	340	345	350	
Tyr	Cys	Ser	Tyr	Val	Pro	His	Val	Arg	Ile	Cys	Met	Pro	Ser	Thr	Asp	355	360	365	

Gly Ile Ser Ser Ser Glu Asp Leu Leu Ala Asn Gly
 370 375 380

<210> 24

<211> 757

<212> PRT

<213> Homo sapiens

<400> 24

Met Thr Ser Gly Ser Val Phe Phe Tyr Ile Leu Ile Phe Gly Lys Tyr
 1 5 10 15

Phe Ser His Gly Gly Gly Gln Asp Val Lys Cys Ser Leu Gly Tyr Phe
 20 25 30

Pro Cys Gly Asn Ile Thr Lys Cys Leu Pro Gln Leu Leu His Cys Asn
 35 40 45

Gly Val Asp Asp Cys Gly Asn Gln Ala Asp Glu Asp Asn Cys Gly Asp
 50 55 60

Asn Asn Gly Trp Ser Met Gln Phe Asp Lys Tyr Phe Ala Ser Tyr Tyr
 65 70 75 80

Lys Met Thr Ser Gln Tyr Pro Phe Glu Ala Glu Thr Pro Glu Cys Leu
 85 90 95

Val Gly Ser Val Pro Val Gln Cys Leu Cys Gln Gly Leu Glu Leu Asp
 100 105 110

Cys Asp Glu Thr Asn Leu Arg Ala Val Pro Ser Val Ser Ser Asn Val
 115 120 125

Thr Ala Met Ser Leu Gln Trp Asn Leu Ile Arg Lys Leu Pro Pro Asp
 130 135 140

Cys Phe Lys Asn Tyr His Asp Leu Gln Lys Leu Tyr Leu Gln Asn Asn
 145 150 155 160

Lys Ile Thr Ser Ile Ser Ile Tyr Ala Phe Arg Gly Leu Asn Ser Leu
 165 170 175

Thr Lys Leu Tyr Leu Ser His Asn Arg Ile Thr Phe Leu Lys Pro Gly
 180 185 190

Val Phe Glu Asp Leu His Arg Leu Glu Trp Leu Ile Ile Glu Asp Asn
 195 200 205

His Leu Ser Arg Ile Ser Pro Pro Thr Phe Tyr Gly Leu Asn Ser Leu
 210 215 220

Ile Leu Leu Val Leu Met Asn Asn Val Leu Thr Arg Leu Pro Asp Lys
 225 230 235 240

Pro Leu Cys Gln His Met Pro Arg Leu His Trp Leu Asp Leu Glu Gly
 245 250 255

Asn His Ile His Asn Leu Arg Asn Leu Thr Phe Ile Ser Cys Ser Asn
 260 265 270
 Leu Thr Val Leu Val Met Arg Lys Asn Lys Ile Asn His Leu Asn Glu
 275 280 285
 Asn Thr Phe Ala Pro Leu Gln Lys Leu Asp Glu Leu Asp Leu Gly Ser
 290 295 300
 Asn Lys Ile Glu Asn Leu Pro Pro Leu Ile Phe Lys Asp Leu Lys Glu
 305 310 315 320
 Leu Ser Gln Leu Asn Leu Ser Tyr Asn Pro Ile Gln Lys Ile Gln Ala
 325 330 335
 Asn Gln Phe Asp Tyr Leu Val Lys Leu Lys Ser Leu Ser Leu Glu Gly
 340 345 350
 Ile Glu Ile Ser Asn Ile Gln Gln Arg Met Phe Arg Pro Leu Met Asn
 355 360 365
 Leu Ser His Ile Tyr Phe Lys Lys Phe Gln Tyr Cys Gly Tyr Ala Pro
 370 375 380
 His Val Arg Ser Cys Lys Pro Asn Thr Asp Gly Ile Ser Ser Leu Glu
 385 390 395 400
 Asn Leu Leu Ala Ser Ile Ile Gln Arg Val Phe Val Trp Val Val Ser
 405 410 415
 Ala Val Thr Cys Phe Gly Asn Ile Phe Val Ile Cys Met Arg Pro Tyr
 420 425 430
 Ile Arg Ser Glu Asn Lys Leu Tyr Ala Met Ser Ile Ile Ser Leu Cys
 435 440 445
 Cys Ala Asp Cys Leu Met Gly Ile Tyr Leu Phe Val Ile Gly Gly Phe
 450 455 460
 Asp Leu Lys Phe Arg Gly Glu Tyr Asn Lys His Ala Gln Leu Trp Met
 465 470 475 480
 Glu Ser Thr His Cys Gln Leu Val Gly Ser Leu Ala Ile Leu Ser Thr
 485 490 495
 Glu Val Ser Val Leu Leu Leu Thr Phe Leu Thr Leu Glu Lys Tyr Ile
 500 505 510
 Cys Ile Val Tyr Pro Phe Arg Cys Val Arg Pro Gly Lys Cys Arg Thr
 515 520 525
 Ile Thr Val Leu Ile Leu Ile Trp Ile Thr Gly Phe Ile Val Ala Phe
 530 535 540
 Ile Pro Leu Ser Asn Lys Glu Phe Phe Lys Asn Tyr Tyr Gly Thr Asn
 545 550 555 560

Gly Val Cys Phe Pro Leu His Ser Glu Asp Thr Glu Ser Ile Gly Ala
565 570 575

Gln Ile Tyr Ser Val Ala Ile Phe Leu Gly Ile Asn Leu Ala Ala Phe
580 585 590

Ile Ile Ile Val Phe Ser Tyr Gly Ser Met Phe Tyr Ser Val His Gln
595 600 605

Ser Ala Ile Thr Ala Thr Glu Ile Arg Asn Gln Val Lys Lys Glu Met
610 615 620

Ile Leu Ala Lys Arg Phe Phe Phe Ile Val Phe Thr Asp Ala Leu Cys
625 630 635 640

Trp Ile Pro Ile Phe Val Val Lys Phe Leu Ser Leu Leu Gln Val Glu
645 650 655

Ile Pro Gly Thr Ile Thr Ser Trp Val Val Ile Phe Ile Leu Pro Ile
660 665 670

Asn Ser Ala Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Arg Pro Phe
675 680 685

Lys Glu Met Ile His Arg Phe Trp Tyr Asn Tyr Arg Gln Arg Lys Ser
690 695 700

Met Asp Ser Lys Gly Gln Lys Thr Tyr Ala Pro Ser Phe Ile Trp Val
705 710 715 720

Glu Met Trp Pro Leu Gln Glu Met Pro Pro Glu Leu Met Lys Pro Asp
725 730 735

Leu Phe Thr Tyr Pro Cys Glu Met Ser Leu Ile Ser Gln Ser Thr Arg
740 745 750

Leu Asn Ser Tyr Ser
755

<210> 25

<211> 11

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 25

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 26

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: internalizing domain derived from HIV tat protein

<400> 26

Gly Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10 15

<210> 27

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 27

tgccaaaaag gatattttcc ctgtgggaat cttta 34

<210> 28

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 28

ctaggaaact ggtttcatta tactgtctcc aagtgttatt ttgttca 47

<210> 29

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: RACE primer

<400> 29

ccatcctaatac gactcact atagggc 27

<210> 30

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: RACE primer

<400> 30

attgtcatct agaattagcc aagttagctg at 32

<210> 31

<211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: RACE primer

 <400> 31
 aacaaggaat ttaatcccgt aaacaag 27

 <210> 32
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: RACE primer

 <400> 32
 actcactata gggctcgagc ggc 23

 <210> 33
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: RACE primer

 <400> 33
 atattccagg tctgagggtt gtgat 25

 <210> 34
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: RACE primer

 <400> 34
 atattccagg tctgagggtt gtgat 25

 <210> 35
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

 <400> 35
 ctgctttgga aatctttttg tca 23

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 36
ttttccaggt cgaatgttac tga 23

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 37
atgccttgct gtggatggag 20

<210> 38
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 38
acttcggtgg acagcatgg 19

<210> 39
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 39
cgtgcagtgc cgcctcatgg 20

<210> 40
<211> 15
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 40

gtcgacggcg agccc

15

<210> 41

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 41

tctttgggac cttgtctgca a

21

<210> 42

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 42

tgggccgcgt ctcctttgag ct

22